

STIC Search Report Biotech-Chem Library

STIC Database Trend ing Number of Security

TO: Minh-Tam Davis

Location: rem/3A24/3C18

Art Unit: 1642

Wednesday, April 26, 2006

Case Serial Number: 09/762577

From: Toby Port

Location: Biotech-Chem Library

REM-1A59

Phone: (571)272-2523

toby.port@uspto.gov

Searen Nores

Dear Examiner Davis,

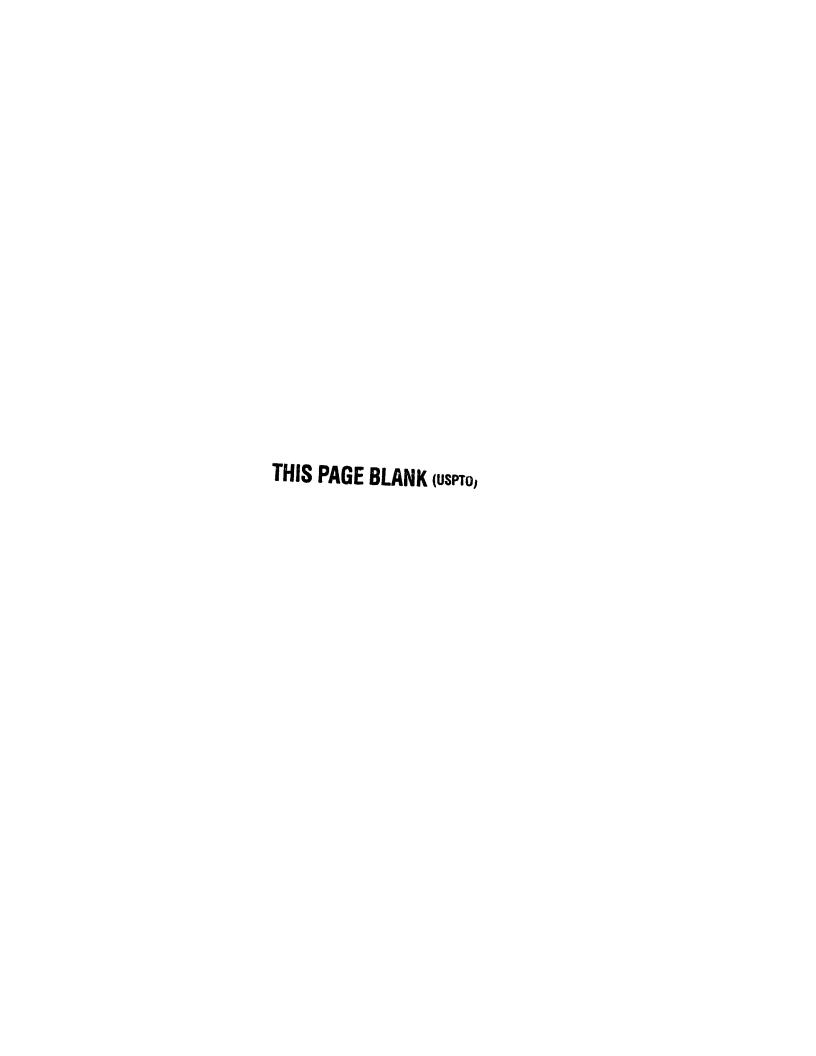
See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port Technical Information Specialist STIC Biotech/Chem Library (571)272-2523





STIC-Biotech/ChemLib

From:

Chan, Christina

Sent:

Thursday, April 20, 2006 6:34 PM

To:

Davis, Minh-Tam; STIC-Biotech/ChemLib

Subject:

RE: Rush search request for 09/762577

Please cosh. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 (571)-272-0841 Remsen, 3E89

----Original Message-----

From:

Davis, Minh-Tam

Sent:

Thursday, April 20, 2006 10:40 AM

To:

Chan, Christina

Subject:

Rush search request for 09/762577

Please search in commercial database, issued patent files, pGPUB and interference:

1) Oligomer search for SEQ ID NO:11

2) Oligomer search for the nucleic acid encoding SEQ ID NO:12.

Thank you.

MINH TAM DAVIS

ART UNIT 1642, ROOM 3A24, MB 3C18

272-0830

Searcher:	
Searcher Phone:	
Date Searcher Picked up:_	
Date completed:	
Searcher Prep Time:	
Online Time:	

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Kasof,G.M. and Gomes,B.C.
Livin, a novel inhibitor of apoptosis protein
J. Biol. Chem. 276 (5), 3238-3246 (2001)
11024045
                                                                                           Kasof,G.M. and Gomes,B.O Direct Submission Submitted (05-OCT-2000)
                                                                                                                                                                                                        Homo
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                                                                                  Submitted (05-OCT-2000) Enabling (AstraZeneca Pharmaceuticals, 1800
                                                                                                                                                                                                 Homo
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                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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        /gene="LIVIN"
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/gene="LIVIN"
                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                           Cocation/Qualifiers
                                                                                                                                                                                                                         GI:11245452
                                                                                                                                                                                                         (human)
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llarity 100.0%;
Conservative
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/note="inhibitor-of-apoptosis family member; contains BIR and COOH-terminal RING finger domains"
/codon_start=1
/product="livin inhibitor-of-apotosis"
/protein_id="AAG33622.1"
/protein_id="AAG33622.1"
/db_xref="G1:11245453"
/translation="MGPKDSAKCLHRGPQPSHWAAGDGPTQERCGPRSLGSPVLGLDTCRAWDHVDGQILGQLRPLTEEEEEEGAGATLSRGPAFPGMGSEELRLASFYDWPLTAE
VPPELLAAAGFFHTGHQDKVRCFFCYGGLQSWKRGDDPWTEHAKWFPSCQFLLRSKGRDVHSYQETHSQLCBSAQDEPGARVSLYPELFTPRREVQSESAQGEPGARVSLGSWDFWEEPEDAAPVAPSVPASGYPELFTPRREVQSESAQGEPGARDVEAQLRRLQEERTCKVCLDRAVSIVFVPCGHLVCAECAPGLQLCPICRAPVRSRVRTFLS"

y Match
98.6%; Score 1228; DB 8; Length 1260;
Local Similarity 100.0%; Pred. No. 0;
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GTCAGAGCCAGTGTTCCCTCCATGGGACCTAAAGACAGTGCCAAGTGCCTGCACCGTGGA CAGGAGCCAGGAGCCAGGGATGTGGAGGCGCGCCAGCTGCAGGAGGAGGACGACG CCTGCCTCTGGGTACCCTGAGCTGCCCACACCCAGGAGAGAGGTCCAGTCTGAAAGTGCC CTGGGCTCCTGGGACCCGTGGGAAGACCGGAAGACGCAGCCCCTGTGGCCCCCTCCGTC TGGAAGCGCGGGGACGACCCCTGGACGGAGCATGCCAAGTGGTTCCCCAGCTGTCAGTTC TTCCACACAGGCCATCAGGACAAGGTGAGGTGCTTCTTCTGCTATGGGGGGCCTGCAGAGC ACCTTGTCCAGGGGGCCTGCCTTCCCCCGGCATGGGCTCTGAGGAGTTGCGTCTGGCCTCC CAGATCCTGGGCCAGCTGCGGCCCCTGACAGAGGAGGAAGAGGAGGAGGAGGCCCCGGGGCCC CAGATCCTGGGCCAGCTGCGGCCCCTGACAGAGGAGGAAGAAGAGGAGGAGGAGGCCCCGGGGCC TCTCTGGGCAGCCCTGTCCTAGGCCTGGAACACCTGCAGAGCCTTGGGATCGG CCACAGCCGAGCCACTGGGCAGCCGGTGATGGTCCCACGCAGGAGCGCTGTGGACCCCGC CCACAGCCGAGCCACTGGGCAGCCGGTGATGGTCCCACGCAGGAGCGCTGTGGACCCCGC AAGGGCCAGCTGGGCATATTCTGAGATTGGCCATCAGCCCCCATTTCTGCTGCAAACCTG GGCAGGCCTGTGCCTATCCCTGCTGTCCCCAGGGTGGGCCCCCGGGGGTCAGGAGCTCCAG TGGAAGCGCGGGGACGACCCCTGGACGGAGCATGCCAAGTGGTTCCCCAGCTGTCAGTTC TTCCACACAGGCCATCAGGACAAGGTGAGGTGCTTCTTCTGCTATGGGGGCCTGCAGAGC ACCTTGTCCAGGGGCCTGCCTTCCCCGGCATGGGCTCTGAGGAGTTGCGTCTGGCCTCC TCTCTGGGCAGCCCTGTCCTAGGCCTGGACACCTGCAGAGCCTGGGACCACGTGGATGGG AAGGGCCAGCTGGGCATATTCTGAGATTGGCCATCAGCCCCCATTTCTGCTGCAAACCTG GGCAGGCCTGTGCCTATCCCTGCTGTCCCCAGGGTGGGCCCCCGGGGGGTCAGGAGCTCCAG 858 812 798 752 692 678 632 618 318 738 572 558 512 498 452 438 392 378 332 272 258 212 198 152 138 92 78

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Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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RIGIN
98.6%; Score 1228; DB 8; Length 1301;
Best Local Similarity 98.6%; Score 1228; DB 8; Length 1301;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                               RS Strausberg, L. Feingold, E.A., Grouse, L.H., Derge, J.G.,
RS Strausberg, L. Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buere, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M. F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D. K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
12,77023
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                                                                                                                Direct Submission
Submitted (17-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                    Strausberg, R
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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cDNA Library Preparation: Rubin Laboratory
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/notte="synonyms: ML-IAP, K
/db xref="GeneID:79444"
/db xref="MIM:605737"
1497..1045
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'db_xref="taxon:9606"
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100.0%; Pr
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
..BC.Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy L Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Mor Teika Olson, Diana Palmquiet, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                   Liao,
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 34 Row: f Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: matched mxNA gi: 21536419. /gene="BIRC7" /codon_start=1 /product="livin inhibitor o /procein_id="AAH14475.1" /db_xref="GI:15680241" /db_xref="GeneID.79444" /db_xref="MIM:605737"
/translation="MCPKDSAKCLHRGPQPSHWAAGDGPTQERCGPRSLGSPVLGLDT
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DFVHSYQETHSQLLGSMDPWESPEDAAPVAPSYPASGYPELFTPRREVQSESAQEFGG
VSPAQAQRAWVLEPGGRAPVEAQLRRLQEERTCKVCLDRAVSIVFVPCGHLVCAECA
PGLQLCPICRAPVRSRVRTFLS" /clone="MGC:23131 IMAGE:4859588" /tissue_type="Skin, melanotic melanoma, /clone_Tib="NIH_MGC_49" /lab_host="DH10B-R" KIAP, LIVIN, RNF50, MLIAP" of apoptosis, isoform

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TCTCTGGGCAGCCCTGTCCCTAGGCCTGGACACCTGCAGAGCCCTGGGACCACGTGGATGGG 318
                                                                                      CCACAGCCGAGCCACTGGGCAGCCGGTGATGGTCCCACGCAGGAGCGCTGTGGACCCCGC
                                                                                                                                                  GTCAGAGCCAGTGTTCCCTCCATGGGACCTAAAGACAGTGCCAAGTGCCTGCACCGTGGA
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AUTHORS
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AY358836
LOCUS
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ORGANISM
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VERSION
KEYWORDS
                                                                                             FEATURES
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                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                         Hominidae; Homo.

22 (Dark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Schen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E., Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P.

The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins:

A Bioinformatics Assessment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 799
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                                                                                                                                                               Direct Submission
                                                                                                                                                                                       Clark, H.F
                                                                                                                                                                                                                                                     Genome Res. 13
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AY358836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                 ed (01-AUG-2003) Department of DNA Way, South San Francisco, Location/Qualifiers
                        /organism="Homo sapiens"
/mol_type="mRNA"
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(10), 2265-2270 (2003)
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Best Local Sim
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/protein_id="AAQ89195.1"
/db_xref="GI:37182790"
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/note="PRO21344"
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/clone="DNA172970"
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Matches 833; Conserv
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

E 1 (bases 1 to 840)
S Tanaka, H. and Kaieda, I.
Survivin-like polypeptide and its DNA
Survivin-like polypeptide and its DNA
CHEMICAL INDUSTRIES LTD, HIROSHI TANAKA, ISAO KAIEDA
OS Homo sapiens (human)
WO 0233071-A/5
PD 25-APR-2002
PF 16-OCT-2001 WO 2001JP009071
PF 16-OCT-2000 JP 00P 316721, 20-DEC-2000 JP 00P 386809 PI
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PF 16-CCT-2001 WO 2001JP009071

PR 17-CCT-2000 JP 00P 316721,20-DEC-2000 JP 00P

HIROSHI TANAKA,ISAO KAIEDA

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PC A61K38/17, A61K39/395, A61K48/00, A61P35/00, A61P43/00
Survivin-like polypeptide and its DNA
FH Key Location/Qualifiers
FT source 1.840
FT /organism='Homo sapiens (human)'.
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BD167853
BD167853.1 GI:27873665
WO 0233071-A/5.
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  GTGCCACCCGAGCTGCTGGCTGCTGCCGGCTTCTTCCACACAGGCCATCAGGACAAGGTG
                                                                                                                      GGCATGGGCTCTGAGGAGTTGCGTCTGGCCTCCTTCTATGACTGGCCGCTGACTGCTGAG
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Tanaka, H. and Kaieda, I.

Survivin-like polypeptide and its DNA
Patent: JP 2002355062-A 5 10-DEC-2002;

TAKEDA CHEMICAL INDUSTRIES LTD
OS Homo sapiens (human)
PD 2002355062-A/5
PD 10-DEC-2002
PF 16-OCT-2001 JP 2001318533
PI HIROSHI TANAKA, ISAO KAIEDA
PC C12N15/09, A61K31/7088, A61K38/55, A611
PC 00, A61P35/00,
PC A61P43/00, A61P43/00, C07K14/82, C07K16
PC C12N1/21,
PC C12N15/10, C12P21/02, C12Q1/02, C12Q1/68
G01N33/53,
PC G01N33/53,
PC G01N33/53, G01N33/566, G01N33/574, C121
CC Survivin-like polypeptide and its D1
FH Key
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FT TOTALLIST / O. C12P1/07, C12P1/08
PC G1N33/50, C12P1/07, C12P1/
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JP 2002355062-A/5.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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p 2002355062-A/5
10-DEC-2002
16-OCT-2001 JP 2001318533
HIROSHI TANAKA, ISAO KAIEDA
C12N15/09, A61K31/7088, A61K38/55, A61K39/395, A61K39/395, A61K48/
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A61P43/00,A61P43/00,C07K14/82,C07K16/32,C12N1/15,C12N1/19,
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Survivin-like polypeptide and its DNA
                                                                                           /organism='Homo
/organism="Homo sapiens'
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Deng,G., Lin,J.H. and Morser,M.J.

DANA encoding human apoptosis inhibitor, protein HIAP3

ALL Referring ARTIENGESELLSCHAFT

ON Homo sapiens (human)

PN JP 2002524039-A/1

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A61K37/02,A61K37/54
A61K37/02,A61K37/54
DNA encoding human apoptosis inhibitor,
Location/Qualifiers
(170). (1066).
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31-JUL-1998 US 09/127928
31-JUL-1998 US 09/127928
GANG DENG, JIING HUEY LIN, MICHAEL JOHN MORSER
C12N15/09, A61K31/7088, A61K35/76, A61K38/00, A61K38/46, A61K45/00,
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Deng,G., Lin,J.-H. and Morser,M.J.
DNA encoding a novel human inhibitor-of-apoptosis
Patent: US 6472172-A 1 29-OCT-2002;
Schering Aktiengesellschaft; Berlin;
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ACCITIGICCAGGGGGCCTGCCTTCCCCGGCATGGGCTCTGAGGAGTTGCGTCTGGCCTCC
              ACCTTGTCCAGGGGGCCTGCCTTCCCCCGGCATGGGCTCTGAGGAGTTGCGTCTGGCCTCC
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nilarity 99.9%;
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Guangzhou Entrepreneur Park for Overseas Chinese Schoi
Baoshi Rd., GETDD, Guangzhou, Guangdong 510730, China
Location/Qualifiers
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Li,H., Ke,R., Wang,C.,
Direct Submission
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Mammalia; Eutheria;
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/product="baculoviral IAP repeat-containing 7"
/protein_id="AsS01729.1"
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                                                                                                                                                                                                           /map="20q13.3"
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                                                                                                                                             gene="BIRC7"
                                                                                                                                                                     note="synonym:
                                                                                                                                                                                    gene="BIRC7"
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Best Local Similarity
Matches 631; Conserv
Hominidae; Homo.

E 1 (bases 1 to 1168)

S Lin,J.-H., Deng,G., Huang,Q. and Morser,J.,

A Novel member of the inhibitor of apoptosis protein fam
L Biochem. Biophys. Res. Commun. (2000) In press

E 2 (bases 1 to 1168)

S Lin,J.-H., Deng,G. and Morser,J.

Direct Submitseion
L Submitted (29-AUG-2000) Cardiovascular Research, Berlex
Inc., 15049 San Pablo Ave., Richmond, CA 94804, USA
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/protein id="AAG37878.1"
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DFVHSVQETHGQLLGSSNDPWESPEDAAPVAPSVPASGYPELFTPRREYQSESAQEPGG
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/mol_type="mRNA"
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ALIGNMENTS

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AC ADH 02-JUL-2002; 2002US-00188646 08-JAN-2004. US2004005565-A1 Homo sapiens hyperproliferative Human Livin DNA. ADH89535; ADH89535 standard; DNA; 1260 Bennett (ISIS-) ISIS PHARM INC 02-JUL-2002; 2002US-00188646 22-APR-2004 ÇF, Dobie KW; (first entry) disorder; aberrant apoptosis; human; ds; Livin; gene. 8₽.

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AAL42857 ADT88075 ADQ25445 ADH89543

Aaal5007 CDNA enco Add.88075 Human pro Add.25445 Human sof Adh.89543 Human Liv Aal42857 Survivin-Aal42856 Survivin-Aal42856 Survivin-Aadh89542 Human SBh Addh89542 Human SBh

The invention relates to an antisense oligonucleotide targeted to nucleic acid encoding Livin and that specifically hybridises with nucleic acid encoding Livin and inhibits expression of Livin. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative disorder or aberrant apoptosis. The presequence represents human livin DNA.

The present

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New antisense oligonucleotide, having a sequence targeted to a nucleic acid encoding Livin, useful for preparing a composition for treating hyperproliferative disorder or aberrant apoptosis.

Example 13; SEQ ID NO 4; 60pp; English.

WPI; 2004-098436/10.

P-PSDB; ADH89685.

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The invention relates to a method of screening for nucleic acid molecules CC that show altered expression in a first cell sample comprising comparing CC that show altered expression in a first cell sample comprising comparing CC sample, where the first sample has been grown in the presence of butyrate CC or a related carbon source from which butyrate is directly or indirectly CC derived, but the reference sample has been grown in the presence of butyrate CC derived, but the reference sample has not. The invention also relates to the initiation and/or progression of colorectal cancer in an animal, CC comprising providing at least one nucleic acid molecule associated with CC comprising providing a biological sample comprising at least one cell to be tested, contacting the sample which binds to at least one nucleic acid and CC nucleic acid molecule) which binds to at least one mucleic acid and CC detecting the presence of at least one molecule in the sample, a method CC and/or progression of colorectal cancer in an animal comprising providing CC a biological sample comprising at least one cell to be tested, contacting CC the sample with at least one ligand that specifically binds at least one polympetide encoded by a nucleic acid or a variant polypeptide comprising CC an amino acid sequence which varies by the addition, deletion or
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cc substitution of at least one amino acid residue and detecting the cc presence of the polypeptide in the sample, a method of screening for cagents that modulate the activity of at least one polypeptide encoded by cancer comprising forming a preparation and/or progression of colorectal cancer comprising forming a preparation comprising at least one polypeptide encoded by a nucleic acid or a variant polypeptide comprising cat least one addition, deletion or substitution and at least one agent to be tested and determining the activity of the agent with respect to comprision identified by the method, for use as a pharmaceutical. The methods are useful for screening for nucleic acid molecules that show a ltered expression in a cell sample, and for detecting a nucleic acid and a polypeptide respectively, that are associated with the initiation can apolypeptide encoded by a gene associated with the initiation can seful for screening for agents that modulate the activity of at least one polypeptide encoded by a gene associated with the initiation cand/or progression of cancer, where agents identified by the methods are useful for treating colorectal cancer. The methods could also be used to detect or monitor other conditions such as colitis, Crohn's disease or concerous growth. This sequence represents a human nucleic acid cancer cancerous growth. This sequence represents a human nucleic acid coldentified by the screening method of the invention.
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CC The present invention describes an isolated nucleic acid molecule, which CC comprises the sequence of any of the genes that are up-regulated or down-cc regulated in specific cancers (e.g. about 1031 genes up-regulated in cc acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer CC abs58521 to ABR58709. Also described: (1) determining the presence or CC absence of a pathological cell in a patient; (2) an expression vector CC comprising the vector; (4) an isolated polypeptide, which is encoded by CC comprising the vector; (4) an isolated polypeptide, which is encoded by CC comprising the vector; (4) an isolated polypeptide, which is encoded by CC comprising the vector; (5) an antibody that specifically binds the polypeptide cof (4); (6) specifically targeting a compound to a pathological cell in a CC patient by administering to the patient the antibody above; and (7) a CC drug screening assay. The nucleic acid is useful as diagnostic markers or CC diagnosing apathology, e.g. cancer (e.g. cancer of the bone marrow, CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases, CC drug screening, particularly for identifying agents for treating these CC pathologies
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Matches 1228;
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Query Match
Best Local Similarity
Matches 1228; Conserv
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Matches 843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel livin polypeptides and pathophysiological disorders melanoma cancer, Alzheimer's
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The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-regulated in specific cancers (e.g. about 1031 genes up-regulated in acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer related gene nucleotide sequences which encode the proteins given in ABR58521 to ABR58709. Also described: (1) determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising a nucleic acid molecule described above; (3) a host cell
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20-SEP-2001;
13-NOV-2001;
08-FEB-2002;
                                                                                                                                                                                                                                                 New genes that are up-regulated or down-regulated in cancers, useful markers for diagnosing e.g. cancer, ischemia or heart diseases, or an therapeutic targets for screening drugs for treating these diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a DNA vaccine effective for eliciting an immune response against cancer cells which comprises a DNA construct operably encoding at least one cancer-associated Inhibitor of Apoptosis-family protein (IAP-family protein) and at least one immunoactive gene product in a pharmaceutical carrier. The invention is useful for treating cancer such as lung cancer, colorectal cancer and melanoma. The present sequence is the human livin alpha splice variant DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New DNA vaccine comprising a cancer-associated Inhibitor of Apoptosis-family protein immunoactive gene product, useful for eliciting an immu response against cancer.
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IAP-family protein; cancer; lung cancer; colorectal cancer; melanoma;
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                                                                                                                                   protein coding
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/parduct= "Survivin-like protein
/product= "No stop codon is given"
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Matches 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention comprises the amino acid and coding sequences of survivin-like proteins. The survivin-like DNA and protein sequences are useful in diagnostics and screening compounds for treating various cancers and apoptosis abnormality, including gene therapy. The present DNA sequence encodes a survivin-like protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 122; 136pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baculovirus IAP repeat domain or RING-finger domain-containing survivin-like polypeptides and encoded DNAs, applicable in diagnosis and screening compounds for treating various cancers and apoptosis abnormality.
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ACACCCAGGAGAGAGGTCCAGTCTGAAAGTGCCCAGGGAGCCAGGAGCCAGGGATGTTGGAG
                                                                                           GTCCACAGTGTGCAGGAGACTCACTCCCAGCTGGTGGGCTCYTGGGACCCGTGGGAAGAA
                                                                                                                                                GGCATGGGCTCTGAGGAGTTGCGTCTGGGCCTCTATGACTGGCCGCTGACTGCTGAG
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                                                                                                                                                                           GAGCATGCCAAGTGGTTCCCCAGCTGTCAGTTCCTGCTCCGGTCAAAAGGAAGAGACTTT
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       Query Match
Best Local Similarity
Matches 792; Conserv
                                                                                                                     The present sequence encodes a human inhibitor of apoptosis protein, designated HIAP3. The protein is characterised by structural features common to the inhibitor of apoptosis protein family. The HIAP3 polypeptides can be used for the treatment of a disease state in a human patient, which is associated with inappropriate apoptosis and the patient is in need of increased levels of the polypeptide. Ribozymes, which target RNA encoding the polypeptide for treatment of inappropriate decreasing levels of the polypeptide for treatment of inappropriate apoptosis. Antisense nucleotide sequences are also useful for decreasing may be useful in treatment of cancer, chronic viral infections, neurodegenerative disorders, chronic heart failure and dysfunctional
                                                                               Sequence 1337 BP;
                                                                                                                                                                                                                                                                                                                                                                                    Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                                New DNA encoding human inhibitor-of-apoptosis regulation of apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inhibitor of apoptosis protein; HIAP3; apoptosis; cancer; c viral infection; neurodegenerative disorder; c heart failure; dysfunctional immune response; ss.
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                                                                                                                                                                                                                                                                                                                                                                                Fig 1; 57pp; English.
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/product= "human inhibitor of apoptosis
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                                                                             231 A;
                   59.6%;
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Query Match

Sequence

ВP;

169 A; 267

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                   The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples and comparing the expression in the first soft tissue sample indicates the of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                     Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                   Example
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                                                                                                                                                                                                                                                                                                                                                                                                                       26-NOV-2002; 2002US-0429739P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human soft tissue sarcoma-upregulated DNA - SEQ ID
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                                                                                                                                                                                                                              SEQ ID NO 8265; 210pp; English.
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RESULT 14
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                                                                                                                                  Human Livin
                                                02-JUL-2002;
                                                                                                                  hyperproliferative
                                                                                                                                                   22-APR-2004
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 Dobie KW;
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                                 2002US-00188646
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                                                                                                                                                                                    DNA;
                                                                                                                  disorder;
                                                                                                                                   DNA
                                                                                                                                                  entry)
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                                                                                                                 apoptosis;
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Best Local Sim
Matches 651;
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P-PSDB;
AAL42857;
                 AAL42857
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1168 BP;
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The invention relates to an antisense oligonucleotide targeted to nucleic acid encoding Livin and that specifically hybridises with nucleic acid encoding Livin and inhibits expression of Livin. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative disorder or aberrant apoptosis. The presequence represents human livin DNA.
                                                                                                                                                                                                                                                                                            Example 15; SEQ ID NO 12; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                   New antisense oligonucleotide, having a sequence targeted to a nucleic acid encoding Livin, useful for preparing a composition for treating hyperproliferative disorder or aberrant apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2004-098436/10.
DB; ADH89686.
                                                      The present
                                                                                                                                                                       the
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Similarity

48.2%;

206 A; 357 C; 393 G; 212

T; 0 ₽,

0 Other;

Conservative

0;

Score 601; DB 12; Pred. No. 3.8e-255; 0; Mismatches 1;

Length 1168; Indels

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Gaps

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760
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601
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                                                                        GAAGAACCGGAAGACGCAGCCCCTGTGGCCCCCTCCGTTCCCTTGCCTCTGGGTACCCCTGAG
                                                                                                                  GACTTTGTCCACAGTGTGCAGGAGACTCACTCCCAGCTGCTGGGCTCTTGGGACCCGTGG
                                                                                                                                  GACTTTGTCCACAGTGTGCAGGAGACTCACTCCCAGCTGCTGGGCTCCTGGGACCCCGTGG
                                                                                                                                                                                             TGGACGGAGCATGCCAAGTGGTTCCCCAGCTGTCAGTTCCTGCTCCGGTCAAAAGGAAGA
                                                                                                                                                                                                                                                                                                GCTGAGGTGCCACCCGAGCTGCTGCTGCTGCCGGCTTCTTCCACACAGGCCATCAGGAC
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                                                        GAAGAACCGGAAGACGCAGCCCCTGTGGCCCCCCTCCGTCCCTGCCTCTGGGTACCCTGAG
                                                                                                                                                                            TGGACGGAGCATGCCAAGTGGTTCCCCCAGCTGTCAGTTCCTGCTCCGGTCAAAAGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                     CCCCTGACAGAGGAGGAGGAGGAGGAGGCCCCCGGGGCCACCTTGTCCAGGGGGCCTGCC
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standard; DNA;

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Query Match
Best Local Simi
Matches 643;
                                                                                                                                                                                                                                                                                                                                                      Sequence 672 BP; 116 A; 216 C; 228 G; 111 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                             The invention comprises the amino acid and coding sequences of survivin-
like proteins. The survivin-like DNA and protein sequences are useful in
diagnostics and screening compounds for treating various cancers and
apoptosis abnormality, including gene therapy. The present DNA sequence
encodes a survivin-like protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baculovirus IAP repeat domain or RING-finger domain-containing survivin-like polypeptides and encoded DNAs, applicable in diagnosis and screening compounds for treating various cancers and apoptosis abnormality.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 85; Page 119-120; 136pp; Japanese.
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P-PSDB; AAO14946.
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20-DEC-2000; 2000JP-00386809
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                                       GGCATGGGCTCTGAGGAGTTGCGTCTGGCCTTCTATGACTGGCCGCTGACTGCTGAG
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Search completed: April 22, 2006, 09:46:00 Job time: 759 secs

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ALIGNMENTS

REFERENCE AUTHORS TITLE VERSION KEYWORDS SOURCE RESULT 1 BU195879 LOCUS DEFINITION FEATURES COMMENT ACCESSION ORGANISM source 1 (bases 1 to 884) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) B0195879 AGENCOURT_8050326 NIH_MGC_112 Hc 5'', mRNA sequence. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP BU195879.1 GI:22709863 EST. found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Unpublished (1999) Contact: Robert Strausberg, Ph.D. Hominidae; Homo. Eukaryota; Metazoa; Mammalia; Eutheria; Homo sapiens BU195879 CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can domo sapiens (human) late: LLCM2328 row: o column: 12 quality sequence stop: 658 Location/Qualifiers Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Homo mRNA sapiens linear EST 04-SEP-2002 CDNA clone IMAGE:6089315 эģ

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REFERENCE
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Hominidae; Homo.

1 (bases 1 to 924)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                            Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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/mol type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:6294748"
/tissue_type="melanotic melanoma, cell line"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: DCTD/DTP
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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       GACCCCGCTCTCTGGGCAGCCCTGTCCTAGGCCTGGACACCTGCAGAGCCTGGGACCACG
                                                                                  ACCGTGGACCACAGCCGAGCCACTGGGCAGCCGGTGATGGTCCCACGCAGGAGCGCTGTG
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                                                      ACCGTGGACCACAGCCGAGCCACTGGGCAGCCGGTGATGGTCCCACGCAGGAGCGCTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="melanotic melanoma, cell line"
/lab host="DHIOB (phage resistant)"
/clome libs="NIH MGC_112"
/clome libs="NIH MGC_112"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
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/db_xref="taxon:9606"
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BQ682897
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2416 row: C column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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1 (bases 1 to 982)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/lab_host="DH10B (phage-resistant)
/clone_lib="NIH_MGC_112"
                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6259145"
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cDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2402 row: d column: 12
High quality sequence start: 13
High quality sequence stop: 667.
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Tissue Procurement: DCTD/DTP
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1 (bases 1 to 945)

NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
GGACAAGGTGAGGTGCTTCTTCTGCTATGGGGGCCTGCAGAGCTGGAAGCGCGGGGACGA
                                                                GACTGCTGAGGTGCCACCCGAGCTGCTGCTGCTGCCGGCTTCTTCCACACAGGCCATCA
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/tissue_type="melanotic melanoma, cell line"
/lab_host="DH108 (phage-resistant)"
/lab_host="DH108 (phage-resistant)"
/clone_lib="NIH MGC 112"
/clone_lib="NIH MGC 112"
/note="Ozgan: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT prinnig. Directionally cloned into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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mol_type="mRNA"

db_xref="taxon:9606"
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AGENCOURT_8185884 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6263255
5', mRNA sequence.
BQ682378
BQ682378.1 GI:21795057
EST.
                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribute on information can
found through the I.M.A.G.E. Consortium/LLNL at:
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                      http://image.llnl.gov
Plate: LLCM2426 row: n column:
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                                                                                                                     /tissue_type="melanotic melanoma, cell line" /lab host="DH10B (phage resistant)" /clone libs="NIH MCC 112" /clone libs="NIH MCC 112" /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6263255"
                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
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99.9%;
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BUI88703
AGENCOURT 7962186 NIH_MGC_112
5', mENA sequence.
BUI88703
  Mammalia; Eutheria;
                            Eukaryota; Metazoa;
                                                                         Homo sapiens (human)
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Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
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2 Homo
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CDNA clone IMAGE:6106302
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2347 row: c column: 07
High quality sequence start: 12 Contact: Robert Strausberg, I Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP 1 (bases 1 to 958)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Unpublished (1999) Hominidae; Homo. Ph.D. Gene Collection (MGC)

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Touchman, J.W.,

for the NEIBank

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              CD6733774 621 bp mRNA linear fs04c01.y2 Human Lens cDNA (Normalized): fs Homo
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Location/Qualifiers
                                                                                                                                                           CTGCTCCGGTCAAAAGGAAGAGACTTTGTCCACAGTGTGCA 659
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/organism="Homo sapiens"
/do xref="taxon:9606"
/db xref="taxon:9606"
/db xref="taxon:9606"
/clone="IMAGE:6106302"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH108 (phage-resistant)"
/clone_lib="NIH MGC 112"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_3:
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_3:
/note="Organ: skin; Tellowing of californed into EcoRI/KhoI sites using the following 5: adaptor:
GCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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Section on Molecular Str
National Eye Institute
6/331, NIH, Bethesda, MI
Tel: 301 402 3452
Fax: 301 496 0078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae; Homo.

1 (bases 1 to 621)

1 (bases 1 to 621)

Wistow,G., Bernstein,S.L., Wyatt,M.K., Behal,A., Touchman,J.W. Bouffard,G., Smith,D. and Peterson,K.

Expressed sequence tag analysis of adult human lens for the NE project: over 2000 non-redundant transcripts, novel genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: graeme@helix.nih.gov
Plate: 04 row: c column: 01
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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Mol. Vis. 8 (4)
AGGAGTTGCGTCTGGCCTCCTTCTATGACTGGCCGCTGACTGCTGAGGTGCCACCCGAGC
                                                                   CCTGGGACCACGTGGATGGGCAGATCCTGGGCCAGCTGCGGCCCCTGACAGAGGAGGAAG
                                                                                                                                            CCTGGGACCACGTGGATGGGCAGATCCTGGGCCAGCTGCGGCCCCTGACAGAGGAGGAAG
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CD673774
CD673774.1 GI:32175505
                                                                                                                                                                                                                                                                       CCAAGTGCCTGCACCGCACAGCCGAGCCACTGGGCAGCCGGTGATGGTCCCACGC
                                                                                                                                                                                                                                                                                                                                                49.8%; Score 621; DE ilarity 100.0%; Pred. No. 1e-Conservative 0; Mismatches
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//clone lib="Minan Lens cDNA (Normalized): fs"
library (by) was normalized by self-subtraction. One
portion of double stranded plasmid DNA representing the
library was linearized by NotI. This NotI digested library
was used as a template for biotinylated RNA synthesis
using SF6 RNA polymerase. Another portion of the double
stranded plasmid library was converted to single-stranded
circles in vitro using Gene II and Exonuclease III (Life
Technologies). Single-stranded DNA (1 mg) was hybridized
(COt 500) with 41 mg of Bio-RNA and vector blocking
oligonucleotides. The hybridized Bio-RNA/ss-circles were
removed by streptavidin:phenol extraction. EST analysis
was performed on the library at the NIH Intramural
Sequencing Center(NISC)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Lens"
/dev_stage="Adult"
/lab_host="EMDH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="fs04c01"
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Pred. No. 1e-297;
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Gaps

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478

418 180 120 298 60

358

Length 621;

33.47

138

90 78 0

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 824)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     824 bp r 602734106F1 NIH_MGC_49 Homo sapiens mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG770578.1
EST.
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High quality sequence stop: 799.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                  http://image.llnl.gov
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/clone="IMAGG:485964"
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/tlissue_type="melanotic melanoma, high MDR (cell line)"
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/clone_lib="MIH_MGC_49"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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s cDNA clone IMAGE:4859641 5',
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Matches 613;
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                                                                                                                                                                                                                                                                                                             BG762467 830 PP 802733911F1 NIH_MGC_49 Homo sapiens
                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                           1 (bases 1 to 830)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                mRNA sequence.
BG762467
BG762467.1 GI:14073120
                                                                                                                                                                                                              Homo sapiens
                                                                Contact: Robert
                                                                                                                                                         Homi
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                                                                                                                                                         nidae;
                                                                                                                                                                                                                               sapiens (human)
     Library Preparation: Ling Hong/Rubin Laboratory
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Query Match
Best Local Similarity
Matches 611; Conserv
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Plate: LLCM1714 row: f column: 03
                                                                                                                                                                                                                                                                             ACCCGAGCTGCTGGCTGCCGGCTTCTTCCACACAGGCCATCAGGACAAGGTGAGGTG
                                                                      TGCCAAGTGGTTCCCCAGCTGTCAGTTCCTGCTCCGGTCAAAAGGAAGAGACTTTGTCCA
                                                                                                    TGCCAAGTGGTTCCCCCAGCTGTCAGTTCCTGCTCCGGTCAAAAGGAAGAGGACTTTGTCCA
                                                                                                                                                          CTTCTTCTGCTATGGGGGCCTGCAGAGCTGGAAGCGCGGGGACGACCCCTGGACGGAGCA
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/lab_host="DH10B (phage-resistant)"
/clone_tib="NIH MGC 49"
/clone_tib="NIH MGC 49"
/note="Torgan: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Torgan: skin; Vector: pOTB7; Directionally cloned
into EcoRI XhoI sites using the following 5' adaptor:
into EcoRI XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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/mol_type="mRNA"
/db_xref="taxon:9606"
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100.0%; Pred. No. 9.9e-293;
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BU172109
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Matches 606
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLCM2356 row: i column: 20
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1 (bases 1 to 956)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian

Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BU172109 956 bp mRNA linear EST 04-SEP-2002
AGENCOURT 7954295 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6109915
5', mRNA sequence.
BU172109 BU172109 GI:22686093
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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              CGGCCCCTGACAGAGGAAGAAGAAGGAGGAGGCGCCGGGGCCACCTTGTCCAGGGGGCCT
                                                                      CTAGGCCTGGACACCTGCAGAGCCTGGGACCACGTGGATGGGCAGATCCTGGGCCAGCTG
                                                                                                    CTAGGCCTGGACACCTGCAGAGCCTGGGACCACGTGGATGGGCAGATCCTGGGCCAGCTG
                                                                                                                                                            GCAGCCGGTGATGGTCCCACGCAGGAGCGCTGTGGACCCCGGTCTCTGGGCAGCCCTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="melanotic melanoma, cell line"
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/clone_lib="NIH_MGC_112"
/clone_lib="NIH_MGC_112"
/note="organ: skin; Vector: pOTB7; Site_1: xhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. DTrectionally cToned
into EcoRI; xhoI sites using the following 5: adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript I RT (Life Technologies). Note: this is a
NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6109915"
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100.0%; Pred. No. 3.1e-290;
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BQ877438
BQ877438.1 GI:22269446
EST.
                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

http://image.llnl.gov

plate: LLCM2331 row: e column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                        quality sequence stop: 580.
Location/Qualifiers
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/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_l12"
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/clone="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. DIrectionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      702
                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6090222"
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AGENCOURT 8095636 NIH_MGC_112

5', mRNA sequence.

BQ877652

BQ877652 GI:22269660
           CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
plate: LLCM2325 row: c column: 06
                                                                                                                            Contact: Robert Strausberg, Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                           1 (bases 1 to 919)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, N
Unpublished (1999)
                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-remail.nih.gov/Tissue Procurement: ATCC/DCTD/DFP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1719 row: a column: 16
High quality sequence stop: 650.
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1 (bases 1 to 652)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
ACCCGAGCTGCTGCCTGCCGCTTCTTCCACACAGGCCATCAGGACAAGGTGAGGTG
                                            GGCTCTGAGGAGTTGCGTCTGGCCTTCTATGACTGGCCGCTGACTGCTGAGGTGCC
                                                                 GGGCTCTGAGGAGTTGCGTCTGGCCTCCTTCTATGACTGGCCGCTGACTGCTGAGGTGCC
                                                                                                       CTGCAGAGCCTGGGACCACGTGGATGGGCAGATCCTGGGCCAGCTGCGGCCCCTGACAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="melanotic melanoma, high MDR (cell line)"
/lab host="DH10B (phage_resistant)"
/clone_llb="NIH MGC 49"
/clone_llb="NIH MGC 49"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. DTrectionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCAGGG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library. | "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road , 4156 MEBRF, Iowa City, IA 5224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 603)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BM696272 603 bp mRNA linear EST 28-FEB-2002 UI-E-DW0-agl-c-11-0-UI.rl UI-E-DW0 Homo sapiens cDNA clone UI-E-DW0-agl-c-11-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics (www.resgen.com).
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        /note=morgan: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-DWO is a cDNA library containing the following tissue(s): lens. The library containing the following tissue(s): lens. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGATTACCGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-DWO-agl-c-11-0-UI"
/tissue_type="lens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-DW0"
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Query Match Best Local Similarity

46.8%; Score 583; DB 3; Length 603; 100.0%; Pred. No. 8.8e-279;

2	118 CCCATTTCTGCTGCAAACCTGGTCAGAGCCAGTGTTCCCTCCATGGGACCTAAAGACAGT
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Db	181 GCCTGGGACCACGTGGATGGGCAGATCCTGGGCCAGCTGCGGCCCCTGACA
Qy	358 GAGGAGGAGGCGCCGGGGCCACCTTGTCCAGGGGGCCTTGCCTTCCCCGGCATGGGCTCT
Db	241 GAGGAGGAGGCCCGGGGCCACCTTGTCCAGGGGGCCTGCCT
9	418 GAGGAGTTGCGTCTGGCCTCCTTCTATGACTGGCCGCTGACTGCTGAGGTGCCACCCGAG
DЬ	301 GAGGAGTTGCGTCTGGCCTCCTTCTATGACTGGCCGCTGACTGCTGAGGTGCCACCCGAG
Qy	478 CTGCTGGCTGCCGGCTTCTTCCACACACGGCCATCAGGACAAGGTGAGGTGCTTCTTC
DЬ	361 CTGCTGGCTGCTGCCGGCTTCTTCCACACAGGGCCATCAGGACAAGGTGAGGTGCTTCTTC
Qy	538 TGCTATGGGGGCCTGCAGAGCTGGAAGCGCGGGGACGACCCCTGGACGAGCATGCCAAG
Dδ	421 TGCTATGGGGGCCTGCAGAGCTGGAAGCGCGGGGACCCCTGGACGGAGCATGCCAAG
γ9	598 TGGTTCCCCAGCTGTCAGTTCCTGCTCCGGTCAAAAGGAGAGACTTTTGTCCACAGTGTG
DЬ	481 TGGTTCCCCAGCTGTCAGTTCCTGCTCCGGTCAAAAGGAAGAGACTTTGTCC
Qγ	658 CAGGAGACTCACTCCCAGCTGCTGGGCTCCTGGGACCCGTGGG 700
DЬ	541 CAGGAGACTCACTCCCAGCTGCTGGGCTCCTGGGACCCGTGGG 583

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	109502,	31552, A	841, App	17272, A	687, App	738, App	14376, A	12881, A	16570, A	16569, A	12788, A	16572, A	16571, A	6, Appli	10070, A	10069, A	6006, Ap	6005, Ap	194640,	194639,	STOSS, W

ALIGNMENTS

US-09-949-016-1949; A

Patent No.

681233

Application US/09949016

; LENGTH: 1260 ; TYPE: DNA ; ORGANISM: Human US-09-949-016-1949 S 밁 δ 밁 Ş 밁 Ş 밁 Ş GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1949 Query Match Best Local Similarity Matches 1227; PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012 153 259 213 199 139 GTCAGAGCCAGTGTTCCCTCCATGGGACCTAAAGACAGTGCCAAGTGCCTGCACCGTGGA 198 93 33 19 79 AAGGGCCAGCTGGGCATATTCTGAGATTGGCCATCAGCCCCCATTTCTGCTGCAAACCTG AAGGGCCAGCTGGGGCATATTCTGAGATTGGCCATCAGCCCCCATTTCTGCTGCAAACCTG 138 GGCAGGCCTGTGCCTATCCCTGCTGTCCCCAGGGTGGGCCCCCGGGGGTCAGGAGCTCCAG GCAGGCCTGTGCCTATCCCTGCTGTTCCCCAGGGTGGGCCCCCGGGGGTCAGGAGCTCCAG CCACAGCCGAGCCACTGGGCAGCCGGTGATGGTCCCACGCAGGAGCGCTGTGGACCCCGC 258 TCTCTGGGCAGCCCTGTCCTAGGCCTGGACACCTGCAGAGCCTGGGACCACGTGGATGGG Conservative 94.5%; O; Mismatches DB 3; <u>بر</u> Length 1260; Indels 0; Gaps 152 272 212 92

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RESULT 2
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IS-Sequence 1, Application U
Patent No. 6472172
GENERAL INFORMATION:
APPLICANT: Deng, Gang
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# APPLICANT: Morser, Michael J
# TITLE OF INVENTION: DNA Encoding a No. 6:
# TITLE OF INVENTION: DVA Encoding HAP3
# FILE REFERENCE: DNA Encoding HAP3
# CURRENT APPLICATION NUMBER: US/99/127,92:
## CURRENT FILING DATE: 1998-07-31
## CURRENT FILING DATE: 1998-07-31
## CURRENT FILING DATE: 1998-07-31
## COURTENT FILING DATE: 2.0
## SOFTWARE: PatentIn Ver. 2.0
## SEQ ID NO 1
## SEQ ID NO 1
## SEQ ID NO 1
## COURTE: DNA
## ORGANISM: Homo sapiens
## CREATION: (170)...(1066)
## US-09-127-928-1
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 13691

LENGTH: 8572

TYPE: DNA

ORGANISM: Human

US-09-949-016-13691
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US-09-949-016-13691
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RESULT 4

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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
SEQ ID NO 66130
                                                                                                                                          ; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66140
                                                                                                                                                                                                                                                                                                                APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 
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; Patent No. 6812339
; GENERAL INFORMATION:
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Query Match 14.0%; Score 175; DB 3; I
Best Local Similarity 100.0%; Pred. No. 2.5e-69;
Matches 175; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                     SEQ ID NO 66140
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TYPE: DNA
ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGTCTGGCCTCCTTCTATGACTGGCCGCTGACTGCTGAGGTGCCACCCGAGCTGCTGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCGCCGGGGCCACCTTGTCCAGGGGGCCTGCCTTCCCCCGGCATGGGCTCTGAGGAGTTG 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACGTGGATGGGCAGATCCTGGGCCAGCTGCGGCCCCTGACAGAGGAGGAAGAGAGGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09949016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                   Length 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND USES
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Sequence 334, Appirm...

Patent No. 6607879

Patent No. 6607879

GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
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                                                                                                                                                                                                       ; CLONE: 14:
US-09-023-655-334
                                                                                                                              Query Match
Best Local Similarity
Matches 218; Conserv
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US-09-023-655-334
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                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: HEREWITH
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION UMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 9A.01
REFERBROE/DOCKET NUMBER: PA.0
TELECOMMUNICATION INFORMATION:
TELECHHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                IMMEDIATE SOURCE:
LIBRARY: KIDNNOT09
CLONE: 1419118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                      ENGTH:
                 421 GAGTTGCGTCTGGCCTCCTTTCTATGACTGGCCGCTGACTGCTGAGGTGCCACCCGAGCTG
                                                                                361 GAGGAGGCCCCGGGCCACCTTGTCCCAGGGGGCCTTGCCTTCCCCGGCATGGGCTCTGAG
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                                                                                                                                                                                                                                                                                             I: 226 base pairs nucleic acid
                                                   GAGGAGGCGCCGGGGCCACCTTGTCCAGGGGGCCTGCCTTCCCCGGCATGGGCTCTGAG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGTGTGCCCCCGGCCTGCAGCTGTGCCCCATCTGCAGAGCCCCCGTCCGCAGCC 601
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                                                                                                                                Conservative
                                                                                                                                                                                                                                                                    linear
                                                                                                                                              13.5%;
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                                                                                                                       Score 168; DB 3; Length 226,
Pred. No. 3.9e-66;
0; Mismatches 1; Indels
0;
                                                                                                                     Gaps
                     480
                                                                                       420
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Sequence 66134, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/247,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-0-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: PRIOR PRIOR FILING DATE: PRIOR FILING 
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US-09-949-016-66139
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-19-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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Best Local Similarity 100.
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID 0 66139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 601
NO 66134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     515 GTGTGCCTGGACCGCGCGTGTCCATCGTCTTTGTGCCGTGCGGCCACCTGGTCTGTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           541 TATGGGGGCCTGCAGAGCTGGAAGCGCGGGGGACGACCCC 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 CTGGCTGCTGCCGGCTTCTTCCACACAGGCCATCAGGACAAGGTGAGGTGCTTCTTCTGC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09949016
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100.0%; Pred. No. 1.2e-56;
Active 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       601
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OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 601;
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; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66134
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                                                                   Query Match
Best Local S
Matches 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
                                                                                                                                                                                                                                                                                                  TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
                                                                                                                                                                     TOPOLOGI.
IMMEDIATE SOURCE:
BLADTUT04
                                                                                                                                                                                                                                                                                                                                NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 8.3%; So
Local Similarity 100.0%; I
hes 103; Conservative 0;
                                                                                                                                                         LIBRARY: BLADTU
CLONE: 1520835
                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                 ENGTH:
                                 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390
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38
                                                               ch 7.5%; Score 94; DB 3; 1 Similarity 100.0%; Pred. No. 1.2e-3 94; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94304
                                                                                                                                                                                                                                            nucleic acid
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                               TGCGGCGGCTGCAGGAGGAGGAGGACGTGCAAGGTGTGCCTGGACCGCGCGTGTCCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGGCCATCAGGACAAGGTGAGGTGCTTCTTCTGCTATGGGGGCCTGCAGAGCTGGAAGC 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGGGGACGACCCCTGGACGGAGCATGCCAAGTGGTTCCCCAG 432
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                                                                                                                                                                                                                                                               200 base pairs
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3174 PORTER DRIVE
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                                                                                                                                                                                                                                                                                                    216:
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Pred. No. 9.7e-37;
0; Mismatches 0;
                                                                                    1.2e-32;
                                                                                                   Length 200,
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97
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RESULT 11
US-09-949-016-66138
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; GENERAL INFORMATION:
; APPLICANT: Cocke, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FO
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US-09-023-655-387
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                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (650) 845-416
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELECHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 31.
STREET: 31.
CITY: PALO ALTO
CTATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
LIBRARY: BLADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: HEREW!
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                                                                                                                                                                                                                     h 7.5%; Score 94; DB 3; L
Similarity 100.0%; Pred. No. 1.2e-32;
94; Conservative 0; Mismatches 0;
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6607879
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                                                                         TCTTTGTGCCGTGCGGCCACCTGGTCTGTGCTGA 131
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3174 PORTER DRIVE
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Sequence 66138, Application US/09949016 Patent No. 6812339 GENERAL INFORMATION:

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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT STLING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-0-08

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

TENTARE: FRESTSEQ for Windows Version 4.0
RESULT 13
US-09-949-016-66135
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SOPTWARE: FastSEQ for Windows Version
SEQ ID NO 66131
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-66131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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                                                                                                                                                                                                  CTGCCGGCTTCTTCCACACAGG 509
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Conservative (
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-00-20
PRIOR PRILING DATE: 2000-10-20
PRIOR PRILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-90-08
PRIOR FILING DATE: 2000-99-08
PRIOR FILING DATE: 2000-99-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 66136
LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

APRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

APRIOR FILING DATE: 2000-10-03

PRIOR PRIOR APPLICATION NUMBER: 60/31,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASESEQ FOR WINDOWS Version 4.0

LENGTH: 601

TYPE: DNA

CDCANTISM: LINNER
                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66136
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US-09-949-016-66136
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Best Local S
Matches 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 66136, Application US/09949016
PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.0%; les 81; Conservation
                                     220 CAGCTGTCAGTTCCTGCTCCGGTCAAAAGGAAGAGACTTTGTCCACAGTGTGCAGGAGAC
                                                                      606 CAGCTGTCAGTTCCTGCTCCCGGTCAAAAGGAAGAGACTTTGTCCACAGTGTGCAGAGAGAC 665
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                                                                                                                                                   81,
                                                                                                                                                                     Similarity
TCACTCCCAGCTGCTGGGCTC 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCACTCCAGCTGCTGGGCTC 519
                                                                                                                                              Conservative
                                                                                                                                  6.5%; Score 81; DB 3; Lv
100.0%; Pred. No. 8.8e-27;
tive 0; Mismatches 0;
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Pred. No. 8.8e-27;
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OF DETECTION AND USES THEREOF
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US-09-049-016-66137

Sequence 66137, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF ITLE OF INVENTION UNDER: US/09/949,016

CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/231,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION UNDER: 60/231,768
PRIOR APPLICATION UNDER: 60/231,768
PRIOR APPLICATION UNDER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION UNDER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION UNDER: 60/231,498
PRIOR APPLICA
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Result
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Maximum DB
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Perfect score:
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6018
6018
4491
4449
366
2311
268
268
1268
1268
944
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seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                Published_Applications_NA_Main:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

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5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

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9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

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US-10-723-860-4448
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US-10-723-803-735-3
US-10-450-763-27355
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Sequence 126316,		Sequence 80, App	Sequence 80, Appl	Sequence 3, Appli	Sequence 7, Appli	Sequence 5, Appli	Sequence 4, Appli	Sequence 7, Appli	Sequence 145257,	Sequence 145256,	Sequence 145255,	Sequence 145257,	Sequence 145256,	Sequence 145255,	Sequence 13132, A	Sequence 145092,	Sequence 145092,	Sequence 14214, A	Sequence 14213, F	Sequence 14214, F	sequence rears, a

ALIGNMENTS

Sequence 4, Application US/10188646
Publication No. US20040005565A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF LIV
FILE REFERENCE: RTS-0373
CURRENT APPLICATION NUMBER: US/10/188,646
CURRENT FILING DATE: 2002-07-02
UNMERC OF SEQ ID NOS: 153

LIVIN EXPRESSION

US-10-188-646-4

SEQ ID NO 4
LENGTH: 1260
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:

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Best Local Similarity 100.0%; Pred. No. 0;

Conservative 0; Mismatches
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LOCATION: (174)...(1016)
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RESULT 2
US-10-807-897-28
Sequence 28, Application US/10807897
Publication No. US20040192631A1
GENERAL INFORMATION:
APPLICANT: Xiang, Rong
APPLICANT: Zhou, He
APPLICANT: Reisfeld, Ralph A.
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ITITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GROWTH AND
ITITLE OF INVENTION: METHODS OF USE THEREOF
PILE REFERENCE: TSRI-874.1
CURRENT APPLICATION NUMBER: US/10/807,897
CURRENT FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/457,009
PRIOR APPLICATION NUMBER: 60/457,009
IPRIOR FILING DATE: 2003-03-24
INUMBER OF SEQ ID NOS: 29
SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0
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Query Match 98.6%; Score 1228; DB 5; Length 1376; Best Local Similarity 100.0%; Pred. No. 0; Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 19 GGCAGGCCTGTGCCTATCCCTGCTGTCCCAGGGTGGGCCCCGGGGGTCAGGAGCTCCAG 78	WS-10-244-586-1 US-10-244-586-1 Sequence 1, Application US/10244586 Publication No. US20030087319A1 GENERAL INFORMATION: APPLICANT: KASOF, GARRETT M. APPLICANT: PROSSER, JUDITH C. APPLICANT: PROSSER, JUDITH C. ITITLE OF INVENTION: NOVEL PROTEIN FILE REFERENCE: DJB/009901/0270799 CURRENT APPLICATION UNMBER: US/10/244,586 CURRENT FILING DATE: 2002-09-16 PRIOR APPLICATION NUMBER: US/9/594,119 PRIOR APPLICATION NUMBER: US/9/594,119 PRIOR FILING DATE: 2000-06-14 PRIOR FILING DATE: 1999-06-15 IPRIOR FILING DATE: 1999-06-15 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1 LENGTH: 1376 TYPE: DNA ORGANISM: HOMO sapiens	Qy 1159 AGGAGGCCCTTGCTTGGCGTGGGGATGGCTTAACTGTACCTGTTTGGATGCTTCTGAAT 1218	Qy 1039 GGGCTCCCTGCCCTCTCTGCCTGTTCTGGACTGTGTTCTGGGCCTGCTGAGGATGGCAG 1098	Oy 919 TGTGCTGAGTGCCCCCGGCCTGCAGCTGCCCCCARCTGCAGAGCCCCCGTCCGCAGC 978	753 CCTGCCTCTGGGTACCCTGAGCTGCCCACACCCAGGAGAGAGA
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Sequence 2, Application US/10244586
; Publication No. US20030087319A1
; GENERAL INFORMATION:
   APPLICANT: COMES, BRUCE C.
   APPLICANT: KASOF, GARRETT M.
   APPLICANT: KASOF, GARRETT M.
   APPLICANT: PROSSER, JUDITH C.
   ITILE OF INVENTION: NOVEL PROTEIN
   FILE REFERENCE: DJB/00991/0270799
   CURRENT APPLICATION NUMBER: US/10/244,586
; CURRENT APPLICATION NUMBER: US/9/594,119
   PRIOR APPLICATION NUMBER: 05/9/594,119
   PRIOR APPLICATION NUMBER: 06/139,291
   NUMBER OF SEQ ID NOS: 12
   SOFTWARE: PatentIn Ver. 2.1
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   LENGTH: 843
   TYPE: DNA
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Publication No. US20040192631A1

GENERAL INFORMATION:

APPLICANT: Xiang, Rong

APPLICANT: Zhou, He

APPLICANT: The Scripps Research Institute

TITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GRO

FILE REFERENCE: TSRI-874.1

CURRENT APPLICATION NUMBER: US/10/807,897

FULS REFERENCE: TSRI-874.1

CURRENT FILING DATE: 2004-03-24

PRIOR APPLICATION NUMBER: 60/457,009

PRIOR FILLY DATE: 2003-03-24

INTHE: DATE: TSRI JOHN

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 1322

TYPE: DNA

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RESULT 6

US-10-235-026-1

(Sequence 1, Application US/10235026

Publication No. US20030082725A1

GENERAL INFORMATION:
APPLICANT: Deng, Gang
APPLICANT: Lin, Jiing-Huey
APPLICANT: Morser, Michael J

TITLE OF INVENTION: DNA Encoding a No. US20030082725A1el Human Inh:
FILE REFERENCE: 50972AUSD1

CURRENT APPLICATION NUMBER: US/10/235,026

CURRENT FILING DATE: 1998-07-31

PRIOR APPLICATION NUMBER: US/127,928

PRIOR FILING DATE: 1998-07-31

NUMBER OF SEQ ID NOS: 7

NUMBER OF SEQ ID NOS: 7
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                                                                                                                                                                  Query Match
Best Local S
Matches 792
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SEQ ID NO 1
LENGTH: 1337
TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: CDS
LOCATION: (170)..(1066)
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                                               AAGGGCCAGCTGGGCATATTCTGAGATTGGCCATCAGCCCCATTTCTGCTGCAAACCTG
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Pred. No. 0;
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APPLICANT: INCYTE PHARMACEUTICALS, II
APPLICANT: TANG, Y. Tom
APPLICANT: YUE, Henry
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: GUGGLER, Karl J.
APPLICANT: CORLEY, Neil C.
                                                                                                                                                                                                                                                                                                                RESULT 7
US-10-839-882-37
US-10-839-882-37
REQUERE 37, Application US/10839882
Publication No. US20040203106A1
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                                      APPLICANT: LAL, Preeti
APPLICANT: AZIMZAI, Yalda
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BAUMING, Yang
APPLICANT: JUNMING, Yang
APPLICANT: SHIH, Leo L.
TITLE OF INVENTION: PROLIFERATION AND APOPTOSIS RELATED PROTEINS
FILE REFERENCE: PF-0619 PCT
CURRENT APPLICATION NUMBER: US/10/839,882
CURRENT FILING DATE: 2004-05-05
PRIOR APPLICATION NUMBER: US/09/807,452
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US/09/807,452
PRIOR APPLICATION NUMBER: US/09/807,452
PRIOR APPLICATION NUMBER: 09/175,737; unassigned; 60/118,559; 09/249,740; unassigned.
   60/154,336
PRIOR FILING DATE: 1998-10-20; 1998-10-20; 1999-02-04; 1999-04-11; 1999-04-11; 1999-04-11; 1999-04-22
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; NAME/KEY: misc_feature
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US-10-839-882-37
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Sequence 8265, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: AZIZ, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions & TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION UMMBER: 60/429,739
PRIOR APPLICATION UMMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
VOMBER OF SEQ ID NOS: 8393
SOFTWARE: Patentin version 3.2
SEQ ID NO 8265
LENGTH: 858
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-723-860-8265
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Sequence 12, Application US/10188646

Publication No. US20040005565A1

GENERAL INFORMATION:
APPLICANT: C. FYANK Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
FILE REFERENCE: RTS-0373
CURRENT APPLICATION NUMBER: US/10/188,646
CURRENT FILING DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 12
LENGTH: 1168
RESULT 10
US-10-203-708-21
/ Sequence 21, Application US/10203708
/ Publication No. US20030149238A1
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; NAME/KEY: CDS
; LOCATION: (1)...(897)
US-10-188-646-12
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Best Local :
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Local Similarity 99.8%;
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Sequence 11, Application US/10188646
Publication No. US20040005565A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN
FILE REFERENCE: RTS-0373
CURRENT APPLICATION NUMBER: US/10/188,646
CURRENT FILING DATE: 2002-07-02
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GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM D.1.C.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50013
CURRENT APPLICATION NUMBER: US/10/203,708
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 60/186,084
PRIOR APPLICATION NUMBER: 60/186
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1068
TYPE: DNA
ORGANISM: Homo sapiens
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b; Pred. No. 2.1e-259;
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EXPRESSION

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RESULT 12

US-10-723-860-4697, Application US/10723860

Feduence 4697, Application US/10723860

Publication No. US20040253606A1

GENERAL INFORMATION:

APPLICANT: Aziz, Natasha

APPLICANT: Ginsburg, Wendy M.

APPLICANT: Zlocnik, Albert

TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

CURRENT APPLICATION NUMBER: US/10/723,860

CURRENT APPLICATION NUMBER: US/10/723,860

CURRENT FILING DATE: 2003-11-26

PRIOR APPLICATION NUMBER: 60/429,739

PRIOR FILING DATE: 2002-11-26

NUMBER OF SEQ ID NOS: 8393

SOFTWARE: PatentIn version 3.2

LENGTH: 449

TYPE: DNA

ORGANISM: Homo sapiens

US-10-723-860-4697
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Best Local Simi
Matches 491;
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SEQ ID NO 11
LENGTH: 4810
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ORGANISM: H. sapiens
FEATURE:
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CURRENT APPLICATION NUMBER: US/10/203,708
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR FILING DATE: 2001-02-14
PRIOR PFLING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FASUSEQ for Windows Version 3.0
SEQ ID NO 22
LENGTH: 769
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Publication No. US20030149238A1
GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM p.l.c.
TITLE OF INVENTION: NOVEL COMPOUNDS
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GCCGGTGATGGTCCCACGCAGGAGCGCTGTGGACCCCGCTCTCTGGGCAGCCCTGTCCTA
                                                         GCCGGTGATGGTCCCACGCAGGAGCGCTGTGGACCCCGCTCTCTGGGCAGCCCTGTCCTA 279
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Conservative 0;
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APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compos
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modu
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR APPLICATION NUMBER: 60/429,739
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SOFTWARE: NUMBER: 676
TYPE: DNA
COGGANISM: Homo saniens
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                                           CCTGCCCCTCTCTGCCTGTTCTGGACTGTTGTTCTGGGCCTGCTGAGGATGGCAGAGCTGG
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CGCACCTTCCTGTCCTAGGCCAGGTGCCATGGCCCAGGTGGGCTGCAGAGTGGGCTC
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                          CCTGCCCCTCTCTGCCTGTTCTGGACTGTGTTCTGGGCCTGCTGAGGATGGCAGAGCTGG
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

FILE REFERENCE: 790C1P3/US

FULLE REFERENCE: 790C1P3/US

CURRENT APPLICATION NUMBER: US/10/450,763

CURRENT FILING DATE: 2003-06-11

PRIOR APPLICATION NUMBER: 09/540,217

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SOFTWARE: CUSCOM

SEQ ID NO 27357

LENGTH: 3782

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIMILAR

LOCATION: (2200)...(2568)

OTHER INFORMATION: apotosis, accession number AF311388, Smith-Waterman Score=641.

FEATURE: NEORMATION: apotosis, accession number AF311388, Smith-Waterman Score=641.
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US-10-450-763-27357
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LOCATION: (1)...(3782)
OTHER INFORMATION: n =
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AGCCGAGCCACTGGGCAGCCGGTGATGGTCCCACGCAGGAGCGCTGTGGACCCCGCTCTC 262
                                                                                                                                                                             TCCTGGGCCAGCTGCGGCCCCTGACAGAGGAGGAAGAAGAGGAGGGCGCCGGGGCCACCT
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 Search completed: April 22, 2006, 10:02:38

 Job time: 987 secs

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Maximum DB
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seq length: 2000000000
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1: /SIDSS/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

2: /SIDSS/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

3: /SIDSS/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

4: /SIDSS/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

5: /SIDSS/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

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7: /SIDSS/ptodata/1/pubpna/USIO_NEW_PUB.seq:*

8: /SIDSS/ptodata/1/pubpna/USIO_NEW_PUB.seq:*

9: /SIDSS/ptodata/1/pubpna/USIO_NEW_PUB.seq2:*

10: /SIDSS/ptodata/1/pubpna/USIO_NEW_PUB.seq2:*

11: /SIDSS/ptodata/1/pubpna/USIO_NEW_PUB.seq3:*

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                                 GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
14 US-11-135-855-21
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8 US-10-310-914A-81063
8 US-10-310-914A-81062
14 US-11-121-849-61906
14 US-11-121-849-61906
14 US-11-121-849-61907
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Sequence 81063, A
Sequence 81062, A
Sequence 61905, A
Sequence 61905, A
Sequence 61905, A
Sequence 61905, A
Sequence 61908, A
Sequence 61919, A
Sequence 61911, A
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Sequence 81046, 34 21 1.7 21 8 US-10-310-914A-81041 Sequence 81046, 34 21 1.7 21 8 US-10-310-914A-81050 Sequence 810650, 36 21 1.7 21 8 US-10-310-914A-81053 Sequence 810650, 36 21 1.7 463 6 US-09-925-065A-780463 Sequence 781938 42 21 1.7 483 6 US-09-925-065A-780463 Sequence 781938 Sequence 781938 Sequence 781938 Sequence 781938 Sequence 781938 Sequence 930654 Seq

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CURRENT APPLICATION NUMBER: US/11/135,855
CURRENT FILING DATE: 2005-05-24
PRIOR APPLICATION NUMBER: US/10/203,708
PRIOR FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 60/186,084
PRIOR FILING DATE: 2000-02-29
PRIOR FILING DATE: 2000-02-29
                                                                                                                                                                                                                                                                                                                                             ; LENGTH: 1068
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-135-855-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SMITHKLINE BEECHAM CORPORATION APPLICANT: SMITHKLINE BEECHAM p.l.c. TITLE OF INVENTION: NOVEL COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 46
                                                                                                                                                                                       160 ATGGGACCTAAAGACAGTGCCAAGTGCCTGCACCGTGGACCAAGCCGAGCCACTGGGCA 219
280 GGCCTGGACACCTGCAGAGCCTGGGACCACGTGGATGGGCAGATCCTGGGCCAGCTGCGG 339
                                                                                              220 GCCGGTGATGGTCCCACGCAGGAGCGCTGTGGACCCCGCTCTCTGGGCAGCCCCTGTCCTA 279
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APPLICANT: SMITHKLINE BEECHAM p.1.c.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50013
CURRENT APPLICATION NUMBER: US/11/135,855
CURRENT FILING DATE: 2005-05-24
PRIOR APPLICATION NUMBER: US/10/203,708
PRIOR APPLICATION NUMBER: US/10/203,708
PRIOR FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR FILING DATE: 2001-02-14
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR APPLICATION NUMBER: 60/186,084
PRIOR APPLICATION NUMBER: 60/186,084
PRIOR PILING DATE: 2000-02-29
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 22
LENGTH: 769
TYPE: DNA
CRGANISM: Homo sapiens
US-11-135-855-22
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US-11-135-855-22
US-11-135-855-22
, Sequence 22, Application US/11135855
, Publication No. US20050255557A1
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Best Local Similarity
Matches 447; Conserv
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CCCCTGACAGAGGAGGAGGAGGAGGGCGCGGGGCCACCTTGTCCAGGGGGCCTGCC
                           CCCCTGACAGAGGAGGAGGAGGAGGGGGGCCCGGGGGCCACCTTGTCCAGGGGGCCTGCC
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ilarity 100.0%;
Conservative (
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; Pred. No. 6.3e-212;
0; Mismatches 0;
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                                                                                                       ; ORGANISM: Human US-10-310-914A-81063
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US-10-310-914A-81063/c
                                                                                                                           Sequence 8163, Application US/10310914A
Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes (
FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3

SEQ ID NO 81063

LENGTH: 26

TYPE: RNA

TYPE: RNA
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                                    Query Match
Best Local S
Matches 26
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; Sequence 81037, Application US/10310914A
; Publication No. US20060003322A1
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 81037
LENGTH: 28
TYPE: RNA
ORGANISM: Human
ORGANISM: Human
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                             2.1%; Score 26; DB ilarity 100.0%; Pred. No. 0.0 Conservative 0; Mismatches
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100.0%; Pred. No.
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US-11-121-849-61904
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                                                                                                                       Sequence 61905, Application US/11121849 Publication No. US20050272080A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 61904
LENGTH: 25
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APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
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CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
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TYPE: DNA
ORGANISM: Homo sapien
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ORGANISM: Human
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25; Conserv
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; ORGANISM: Homo sapien 
US-11-121-849-61907
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US-11-121-849-61906
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; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-61905
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PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 61906
LENGTH: 25
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Publication No. US20050272080A1
GENERAL INFORMATION:
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Publication No. US20050272080A1
GENERAL INFORMATION:
Query Match 2.0%; Score 25;
Best Local Similarity 100.0%; Pred. No.
Matches 25; Conservative 0; Mismatci
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Best Local Similarity 100.0%; Pred. No.
Matches 25; Conservative 0; Mismatc
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PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator
SEQ ID NO 61305
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Matches 25; Conserva
                                                                                                                                                                                                                      TITLE OF INVENTION: Methods of Genetic Analysis
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
PRIOR FILING DATE: 2004-05-03
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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TITLE OF INVENTION: Methods of Genetic Analysis
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
                                                                                                                          LENGTH: 25
TYPE: DNA
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100.0%; Pred. No. 0.0
tive 0; Mismatches
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                                       Length 25;
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US-11-121-849-61910
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US-11-121-849-61909
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                          Sequence 61910, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
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US-11-121-849-61908
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TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT PILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2004-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
UNMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 61909
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Best Local
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Best Local Similarity 100.0%;
Matches 25; Conservative
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FILE REFERENCE: 3664.1

CURRENT APPLICATION UNMBER: US/11/121,849

CURRENT FILING DATE: 2005-05-03

PRIOR APPLICATION UNMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTMARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 61908
    TITLE OF INVENTION: Methods of Genetic Analysis of
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Publication No. US20050272080A1
GENERAL INFORMATION:
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ORGANISM: Homo sapien
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.ve 0; Mismatches
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Pred. No. 0.085;
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. 0.085;
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Fixed Paraffin Embedded
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; ORGANISM: Homo sapier
US-11-121-849-61912
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US-11-121-849-61912, Application US/11121849

Publication No. US20050272080A1

GENERAL INFORMATION:
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; ORGANISM: Homo sapien
US-11-121-849-61911
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US-11-121-849-61911
; Sequence 61911, Application US/11121849
; Publication No. US20050272080A1
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                                            APPLICATION PAIMA
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
PRIOR FILING DATE: 2004-05-03
NUMBER: Microarray Probe Sequence Listing Generator V 1.1
SDCTWARE: Microarray Probe Sequence Listing Generator V 1.1
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PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 61911
LENGTH: 25
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Best Local
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APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION UNMEER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
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Best Local Similarity
Matches 25; Conserv
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LENGTH: 25
                                  LENGTH: 25
TYPE: DNA
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FILE REFERENCE; 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE; 2005-05-03
PRIOR APPLICATION NUMBER; 60/567,949
PRIOR FILING DATE; 2004-05-03
NUMBER OF SEQ ID NOS: 673904
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RESULT 15
US-11-121-849-61913
| Sequence 61913, Application US/11121849
| Publication No. US20050272080A1
| GENERAL INFORMATION:
| APPLICANT: John Palma
| TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
| TITLE OF INVENTION: Microarrays
| FILE REFERENCE: 3684.1
| CURRENT APPLICATION NUMBER: US/11/121,849
| CURRENT APPLICATION NUMBER: US/11/121,849
| CURRENT FILING DATE: 2005-05-03
| PRIOR APPLICATION NUMBER: 60/567,949
| PRIOR FILING DATE: 2004-05-03
| NUMBER OF SEQ ID NOS: 673904
| SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
| SEQ ID NO 61913
| LENGTH: 25
| TYPE: DNA
| ORGANISM: Homo sapien
Search completed: April 22, 2006, 09:51:10 Job time: 705 secs
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-Q-/Abss/ABSSWEB_spool/US09762577/runat_24042006_105921_763/app_query.fasta_1
-DB=GenEmb1 -QFMT=fastap -SUFFIX=p2noli.rge -MINWATCH=0.1 -LOOPGL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=oligo -TRAMS=human40.cdi -LIST=45
-DCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06p
-USER-US09762577_9CGN 1 _7415_grunat_24042006_105921_763 -NCPU=6 -ICPU=3
-NORMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
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BD167853 Survivin-
BD185365 Survivin-
AX067716 Sequence
                                                                               Description
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	COMMENT	REFERENCE AUTHORS TITLE JOURNAL	KEYWORDS SOURCE ORGANISM	RESULT 1 BD167853 LOCUS DEFINITION ACCESSION VERSION
ROS 2N1	TAKEDA CHEMICAL INDUSTRIES LTD,HIROSHI TANAKA,ISAO KAIEDA OS Homo sapiens (human) PN WO 0233071-A/5 PD 25-APR-2002 PF 16-OCT-2001 WO 2001JP009071	1 (bases 1 to 840) Tanaka, H. and Kaieda, I. Survivin-like polypeptide and its DNA Patent: WO 0233071-A 5 25-APR-2002;	WO 0233071-A/5. Homo sapiens (human) Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	BD167853 BD167853 BD167853 BD167853 BD167853.1 GI:27873665

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PC A61K38/17,A61K39/395,A61K48/00,A61P35/00,A61P43/00

Survivin-like polypeptide and its DNA

FH Key Location/Qualifiers

FT source 1. .840

FT /organism='Homo sapiens (human)'.
AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGluCysAlaProGly
                                                                                      ValGluAlaGlnLeuArgArgLeuGlnGluGluArgThrCysLysValCysLeuAspArg
                                                                                                                                             CTGCCCACACCCAGGAGAGAGGTCCAGTCTGAAAGTGCCCAGGAGCCAGGAGCCAGGGAT
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Qy 8	Db 18	Qy 6	Qy 41 Db 121	Qy 2 Db 6	D Q	US-09-762-57	Alignment Sc. Pred. No.: Score: Percent Simi. Best Local S. Query Match: DB:	FEATURES Source ORIGIN				COMMENT	AUTHORS TITLE JOURNAL	, 9	VERSION KEYWORDS SOURCE	RESULT 2 BD185365 LOCUS DEFINITION ACCESSION	Db 7	0у 2	Db 7
1 PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100	1 CCCCTGACAGAGGAGGAAGAAGGAGGGCGCCGGGGCCACCTTGTCCAGGGGGCCTGCC 2	1 ProLeuThrGluGluGluGluGluGluGlyAlaGlyAlaThrLeuSerArgGlyProAla 8	1 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60	21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40	1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20	77B-12 (1-309) x BD185365 (1-840)	cores: 3.5e-272 Length: 840 280.00 Matches: 280 ilarity: 100.0% Conservative: 0 Similarity: 100.0% Mismatches: 0 90.6% Indels: 0 6 Gaps: 0	iens" DNA"	PC G01N33/53,G01N33/566,G01N33/574,C12N15/00,C12N5/00,A61K37/64 PC Survivin-like polypeptide and its DNA FH Key Location/Qualifiers FT source 1.840 FT /organism='Homo sapiens (human)'.	C12N1/21, 07, MOLEMS/VV, CV/K14/82, CV/K16/32, C12N1/15, C12N1/19, PC C12N1/21, C12P21/02, C12Q1/68, G01N33/15, G01N33/50, PC G01N33/53	33 EDA 61K38/55,A61K39/395,A61K39/395,A61K4	OS Homo sapiens (human) PN JP 2002355062-A/5 PD 10-DEC-2002	Tanaka,H. and Kaieda,I. Survivin-like polypeptide and its DNA Survivin-like polypeptide and its DNA Patent: JP 2002355062-A 5 10-DEC-2002; TAKEDA CHEMICAL NUISEPTER IFFE	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	BD18365.1 GI:31877565 BD18365.1 GI:31877565 UP 2002155062-A/5.	BD185365 Survivin-like polypeptide and its DNA.	81 CTGCAGCTGTGCCCCATCTGCAGAGCCCCCGTCCGCAGCCGTGCGCACCTTCCTGTCC	61 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 2	721 GCCGTGTCCATCGTCTTTGTGCCGTGCGGCCACCTGGTCTGTGCTGAGTGTGCCCCCGGC 780

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Livin; inhibitor-of-apoptosis protein-3
Patent: WO 0077201-A 21-DEC-2000;
AstraZeneca AB (SE)
                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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Homo sapiens
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                                                                                                              /organism="Homo sapie:
/mol_type="unassigned
/db_xref="taxon:9606"
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Sequence 11
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Butz,K., Crnkovic-Mertens,I. and Hoppe-Seyler,F.
LIVIN-SPECIFIC SIRNAS FOR THE TREATMENT OF THERAPY-RESISTANT
Patent: WO 2004091388-A 11 28-OCT-2004;
Deutsches Krebsforschungszentrum Stiftung des oeffentliche n
                                                        Eukaryota;
Mammalia; I
                                                                                                                                                                               LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer
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Patent: WO 2005054507-A 103
University of Sheffield (GB)
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Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Kasof,G.M. and Gomes,B.C.
Livin, a novel inhibitor of apoptosis protein
J. Biol. Chem. 276 (5), 3238-3246 (2001)
11024045
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Kasof,G.M. and Gomes,B.C.
Direct Submission
Submitted (05-OCT-2000) Enabling Science and Technology,
AstraZeneca Pharmaceuticals, 1800 Concord Pike, Wilmington,
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DFVHSYQETHSQLLGSWDPWEEPEDAAPVABSVPASGYPELTTPRREVQSESAQEPGA
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                                                                                                                                                                                                                                                                                                               /gene="LIVIN"
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174. .1016
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/mol_type="mRNA"
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                                                                                                            Homo sapiens of AY358835
AY358835.1 GI
1 (bases 1 to 1301)
Clark, H.F., Gurney, A.L., At
Chen, J., Chow, B., Chui, C.,
                                                                                Homo sapiens (human)
Homo sapiens
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                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                          Homo.
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clone DNA142232
                                                    Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
Abaya,E., Baker,K., Baldwin,D.,
., Crowley,C., Currell,B., Deuel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (01-AUG-2003) Department of Bioinformatics, Inc., 1 DNA Way, South San Francisco, CA 94080, USA Location/Qualifiers
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AlaGluValProProGluLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp
                                                                              PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr
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                                                                                                                                                         ProLeuThrGluGluGluGluGluGluGlyAlaGlyAlaThrLeuSerArgGlyProAla
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RDVEAQLRRLQEERTCKVCLDRAVSIVFVPCGHLVCAECAPGLQLCPICRAPVRSRVR

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/note="PRO19607"
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/mol_type="mRNA"
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/clone="DNA142232"
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AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu
                                         ATGGGACCTAAAGACAGTGCCAAGTGCCTGCACCGTGGACCACAGCCGAGCCACTGGGCA
                                                        MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla
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Hominidae; Homo.

1 (bases 1 to 672)
Tanaka,H. and Kaieda,I.
Survivin-like polypeptide and its DNA
Patent: WO 0233071-A 4 25-ARR-2002;
TAKEDA CHEMICAL INDUSTRIES LTD,HIROSHI TA
OS Homo sapiens (human)
PN WO 0233071-A/4
PD 25-APR-2002
PF 16-OCT-2001 WO 2001JP009071
PR 17-OCT-2000 JP 00P 316721,20-DEC-2
HIROSHI TANAKA,ISAO KAIEDA
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                                           LeuProThrProArgArgGluValGlnSerGluSerAlaGlnGluProGlyAla
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/mol_type="genomic DNA"
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US-09-762-577B-12 (1-309) x BD185364 (1-672)
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1 (bases 1 to 672)

1 TANAKA, H. and Kaieda, I.

Survivin-like polypeptide and its DNA
PAREDA CHEMICAL INDUSTRIES LTD

OS Homo sapiens (human)

PN JP 2002355062-A, 4

PD 10-DEC-2002

PF 16-OCT-2001 JP 2001318533

PI HIROSHI TANAKA, ISAO KAIEDA

PC C12N15/09, A61K31/7088, A61K38/55, A61K

PC 00, A61P35/00,

PC 00, A61P35/00, C07K14/82, C07K16

PC C12N12/1,

PC C12N3/53, G01N33/566, G01N33/574, C12N

CC Survivin-like polypeptide and its DN

FH Key

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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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{\tt LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro}
                                               GÉTGAGGTGCCACCCGAGCTGCTGCTGCCGGCTTCTTCCACACAGGCCATCAGGAC
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Survivin-like polypeptide and its DNA
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Survivin-like polypeptide and its DNA
Patent: WO 0233071-A 3 25-APR-2002;

TAKEDA CHEMICAL INDUSTRIES LTD, HIROSHI TANAKA, ISAO KAIEDA
OS Homo sapiens (human)
PN WO 0233071-A/3
PD 25-APR-2002
PF 16-OCT-2001 WO 2001JP009071
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       ATGGGGCCTAAAGACAGTGCCAAGTGCCTGCACCGTGGACCACAGCCGAGCCACTGGGCA
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17-CCT-2000 JP 00P 316721, 20-DEC-2000
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Tanaka, H. and Kaieda, I.

Survivin-like polypeptide and its DNA
Patent: JP 2002355062-A 3 10-DEC-2002;

TAKEDA CHEMICAL INDUSTRIES LTD
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BD185363.1 GI:31877563
JP 2002355062-A/3.
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                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
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JP 200235502-A/3
10-DEC-2002
16-OCT-2001 JP 2001318533
HIROSHI TANAKA, ISAO KAIEDA
C12N15/09, A61K31/7088, A61K38/55, A61K39/395, A61K39/395, A61K48/00, A61P35/00,
                                                                                                   C12N5/10, C12P21/02, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50,
                                                   G01N33/53,G01N33/566,G01N33/574,C12N15/00,C12N5/00,A61K37/64
Survivin-like polypeptide and its DNA
                                                                                                                                 A61P43/00, A61P43/00, C07K14/82, C07K16/32, C12N1/15, C12N1/19,
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/organism='Homo sapiens
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      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                      Homo sapiens
                                                      Homo sapiens
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/mol_type="genomic DNA"
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SOURCE ORGANISM

Homo sapiens

KEYWORDS

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Lin,J.-H., Deng,G. and Morser,J.
Direct Submission
Submitted (29-AUG-2000) Cardiovascular
Inc., 15049 San Pablo Ave., Richmond, C
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae; Homo.

1 (bases 1 to 1168)

Lin, J.-H., Deng,G., Huang,Q. and Morser,J.

A Novel member of the inhibitor of apoptosis protein Biochem. Biophys. Res. Commun. (2000) In press
                    LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
                                                                                                                                                                                                                                                                                                                                                                                                          MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla
AAGGTGAGGTGCTTCTTCTGCTATGGGGGCCTGCAGAGCTGGAAGCGCGGGGACGACCCC
                                                                                        AlaGluValProProGluLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
                                                                                                                                                  PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr
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|mol_type="mRNA"
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LIVIN-SPECIFIC siRNAS FOR THE TREATMENT OF THERAPY-RESISTANT
Patent: WO 2004091388-A 10 28-OCT-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10 from Patent CQ896990 CQ896990.1 GI:55581832
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Mammalia; Eutheria;
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                                                                                                       ProLeuThrGluGluGluGluGluGlyAlaGlyAlaThrLeuSerArgGlyProAla
                                                                                                                                                             GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg
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AlaGluValProProGluLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp
                                                  PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
                                                                                   CCCCTGACAGAGGAGGAAGAGGAGGAGGAGGCGCCGGGGCCACCTTGTCCAGGGGGCCTGCC
                                                                                                                                                                                                   GCCGGTGATGGTCCCACGCAGGAGCGCTGTGGACCCCGCTCTCTGGGCAGCCCTGTCCTA
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                                                                                                                                             GGCCTGGACACCTGCAGAGCCTGGGACCACGTGGATGGGCAGATCCTGGGCCAGCTGCGG
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/mol_type="unassigned DN/
/db_xref="taxon:9606"
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altechul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
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                                                                                                                                                                   Direct Submission

Submitted (17-SEP-2001) National Institutes of Health, Mammalian Submitted (17-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Janob Sethesda, MD 20892-2590,
                                               NIH-MGC Project URL: http://mgc.no
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Library Preparation: Rubin Laboratory
Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 34 Row: f Column: 10 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21536419. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Sequencing by: Genome Sequence Centre
BC Cancer Agency, Vancouver, BC, Canada
ProLeuThrGluGluGluGluGluGlyAlaGlyAlaThrLeuSerArgGlyProAla 80
                                                                                                                                                                       GCCGGTGATGGTCCCACGCAGGAGCGCTGTGGACCCCGCTCTCTGGGCAGCCCCTGTCCTA
                                                                                                                                                                                                                                                                          ATGGGACCTAAAGACAGTGCCAAGTGCCTGCACCGTGGACCACAGCCGAGCCACTGGGCA
                                                                                                                                                                                                                                                                                                                       MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
                                                                                                  GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg
                                                                       GGCCTGGACACCTGCAGAGCCTGGGACCACGTGGATGGGCAGATCCTGGGCCAGCTGCGG
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DFVHSVQETHSQLLGSWDPWEEPEDAAPVAPSVPASGYPELPTPRREVQSESAQEPGG
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149. .1045
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Matches:
Conservative:
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Indels:
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Search Job ti	B &) B &	g dy	g Qy	망양	Db Qy	B &
Search completed: April 24, 2006, 11:57:50 Job time : 4452 secs	7 201 LeuProThrProArgArgGluValGlnSerGluSerAlaGlnGluProGly 217	181 689	Y 161 AspPheValHisSerValGinGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180 	Y 141 TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160 	Y 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140	Y 101 AlaGluValProProGluLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120 	Y 81 PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100

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Result
No.
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-Q-/abss/ABSSWEB_spool/US09762577/runat 24042006_105917_692/app_query.fasta_1
-Q-/abss/ABSSWEB_spool/US09762577/runat 24042006_105917_692/app_query.fasta_1
-DB=N_Geneseq_-QFMT=fastap_-SUFITIx=p2noTi.rng_-MTNMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-abits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
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-USER=US09762577_GCGN_1 1 727_@runat 24042006_105917_692 -NCPU=6 -ICPU=3
-NO_MAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -FGAPOP=60 -FGA
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                 Score
         280
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1: geneseqn19
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Ygapext 60.0
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   AAL42858
AAF24857
2 ADH89535
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2809.536 Million cell updates/sec
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Aa142858 Survivin-
Aaf24857 Nucleotid
Adh89535 Human Liv
Aea36171 Human nuc
                                                                                                                                                           Description
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14	14	14	14	14	14	14	15	18	21	28	30	30	30	30	44	44	47	54	65	83	87	116	117	120	120	131	149	149	177	217	217	217	217	217	217	218		8	280	
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AAT70841	AEA17853	ADS83238	ADI31171	AAT43709	ABX42884	ADD32333	ADQ51993	ADF17464	ADH93056	AAS91551	ADS83128	ADI55414	ADI31061	ACA55618	ADS83075	ADI31008	AAL42855	AAF66690	ADQ21628	AAL42854	AEA39481	AAS91553	٠.	AAH99228	AAS91550	ADQ25445	AAD16365	ADQ21877	AAD16364	ADT88075	AAA15007	AAZ61210	ADS71344	ACC72843	ADH89543	AAL42856	AAL42857	₩	7.	ACC72844
Aat70841 Mouse apo	17853 Human	Ads83238 Human lym	171 Human	9 Human i	Sovine	Human	Novel		6 Human	DNA enc	8 Human	Adi55414 Human pol	Human	Mouse	Human	Adi31008 Human cDN	Aal42855 Survivin-	z		Aal42854 Survivin-		н	Adh89542 Human Liv			Adq25445 Human sof	Aad16365 Human SBh		T	75	5007	1210 DNA enc	4 Human	343 Human	343	σ	7	24856 Nucleot	Ads71346 Human liv	Acc72844 Human can

ALIGNMENTS

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AAL42858
ID AAL42858 standard; DNA; 840 BP.

XX
AC AAL42858;
XX
DT 05-AUG-2002 (first entry)
XX
DE Survivin-like protein coding sequence 5.
XX
KW Survivin-like protein; diagnosis; screening; cancer; gene; ds;
XX
KW apoptosis abnormality; gene therapy.
XX
OS Unidentified.
XX
PFT CDS 1..840
FTT CDS 1..840
FTT /porduct= "Survivin-like protein 5"
FTT /porduct= "Survivin-like protein 5"
FTT /porduct= "No stop codon is given"
XX
PN WO200233071-A1.
XX
PFT 16-OCT-2001; 2001WO-JP009071.
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Best Local Similarity:
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like proteins. The survivin-like DNA and protein sequences are useful in
diagnostics and screening compounds for treating various cancers and
apoptosis abnormality, including gene therapy. The present DNA sequence
encodes a survivin-like protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baculovirus IAP repeat domain or RING-finger domain-containing survivin-like polypeptides and encoded DNAs, applicable in diagnosis and screenin compounds for treating various cancers and apoptosis abnormality.
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P-PSDB; AAO14947.
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                                                                    AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp
                   GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu
                                                                                                       TGGACGGAGCATGCCAAGTGGTTCCCCCAGCTGTCAGTTCCTGCTCCGGTCAAAAGGAAGA
                                                                                                                          TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg
                                                                                                                                                            AAGGTGAĞGTĞCTTCTTCTĞCTATĞĞĞĞĞCCTĞCAĞAĞCTĞĞAAĞCĞCĞĞĞĞAÇĞAÇÇÇ
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                                                     The present sequence encodes a human polypeptide, designated livin. Livin is an inhibitor of apoptosis protein 3 (IAP-3). Livin is present in certain cancer cell lines and prevents apoptosis. The livin polypeptide is useful for identifying compounds that inhibit and modulate livin function and activity. Such compounds that inhibit and modulate livin dysfunctional apoptosis condition. Livin polypeptides are useful as a source of probes and primers, and in gene therapy. Livin polypeptides and polymucleotides, their inhibitors and modulators are useful for treating pathophysiological disorders related to apoptosis, cancers, particularly melanoma cancer, Alzheimer's disease and Parkinson's disease
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                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                 The invention relates to an antisense oligonucleotide targeted to nucleic acid encoding Livin and that specifically hybridises with nucleic acid encoding Livin and inhibits expression of Livin. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative disorder or aberrant apoptosis. The presquence represents human livin DNA.
                                                                                                                                                                                                                                                                                                                                                                                       New antisense oligonucleotide, having a sequence targeted to a nucleic acid encoding Livin, useful for preparing a composition for treating hyperproliferative disorder or aberrant apoptosis.
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02-JUL-2002;
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P-PSDB;
                                                                                                               08-JAN-2004
                                                                                                                                  US2004005565-A1
                                                                                                                                                                         hyperproliferative
                                                                                                                                                                                            Human Livin
2004-098436/10.
)B; ADH89685.
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                                                  PHARM INC
                                                                                          2002US-00188646
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                                                                                                                                                                          disorder;
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Sequence 1260 BP; 201 A; 398 Ç 421 <u>و</u> 240 ;; 0 Ç 0 Other;

13; SEQ ID NO 4;

60pp; English.

US-09-762-577B-12 : Local S: :y Match: Similarity: cal Similarity: (1-309) x ADH89535 3.62e-257 280.00 100.0% 100.0% 90.6% (1-1260)Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 1260 280 0 0

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                                                                                                                                                                  MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla
                          LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro
                                                                     PheProGlyMetGlySerGluGluLeu&rgLeu&laSerPheTyrAspTrpProLeuThr
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standard;
                                                            LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer
                                          GCCGTGTCCATCGTCTTTGTGCCGTGCGGCCACCTGGTCTGTGCTGAGTGTGCCCCCCGGC
                                                                                                                AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGluCysAlaBroGly
                                                                                                                                               GTGGÄGGCGCAGCTGCGGCGGCTGCAGGAGGAGGACGTGCAAGGTGTGCCTGGACCGC
                                                                                                                                                                    ValGluAlaGlnLeuArgArgLeuGlnGluGluArgThrCysLysValCysLeuAspArg
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DNA; ВP

25-AUG-2005 (first entry)

Human nucleic acid sequence #103

gastrointestinal-gen.; Screening, gene expression, colorectal tumor, colitis, Crohns disease, irritable bowel syndrome, gastrointestinal disease, cytostatic, antiinflammatory; ds.

WO2005054507-A2

03-DEC-2004; 2004WO-GB005078.

04-DEC-2003; 2003GB-00028048

(UYSH-) UNIV SHEFFIELD

Corfe B Chirakkal H;

WPI; 2005-435407/44.

Screening for nucleic acid molecules exhibiting altered expression in cells grown in the presence of butyrate, and detection of the nucleic acid molecules or the encoded polypeptides in diagnosing colorectal

Disclosure; Page 143; 266pp; English.

RESULT 4
ARAJ6171
ID ARAJ
XX ARAJ6171
AC ARAJ617
AC sample, where or a related derived, but invention relates to a method of screening for nucleic actd motecutes t show altered expression in a first cell sample comprising comparing gene expression profile of the sample with that of a second reference ple, where the first sample has been grown in the presence of butyrate a related carbon source from which butyrate is directly or indirectly the researce sample has not. The invention also relates to

> cc a method of detecting at least one nucleic acid molecule associated with cc comprising providing a biological sample comprising at least one cell to comprising providing a biological sample comprising at least one cell to comprising providizing cc detecting the presence of at least one molecule in the sample, a method cc and/or progression of colorectal cancer in an animal comprising providizing cc and/or progression of colorectal cancer in an animal comprising providing cc and/or progression of colorectal cancer in an animal comprising providing cc the sample with at least one polypeptide associated with the initiation cc the sample with at least one ligand that specifically binds at least one can amino acid sequence which varies by the addition, delection or comprising providing the presence of the polypeptide on a propertied and detecting the presence of the polypeptide of a concercial concerci

1260 BP; 201 A; 398 C; 421 G; 240 T; 0 U; 0 Other;

CB:	Mary March:	Desc boost similarity:	10001	+	Score:	Pred. No.:	Alignment Scores:
14	90.6%	100.0%	T00.0%	100.00		3.62e-257	
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US-09-762-577B-12 (1-309) x AEA36171 (1-1260)

Qy 101 Db 474	Db 414	Db 354	γQ	Db 294	Q	Db 234	Ş	DЪ	Qy
AlaGluValProProGluLeuLeuAlaAlaAlaGlyPhePheHigThrGlyHigGlnAsp	TICCCCGGCATGGCTCTGAGGAGTTGCGTCTGGCCTCCTTCTATGACTGGCCGCTGACT	CCCCTGACAGAGGAGGAGAGAGGAGGCCCCGGGCCACCTTGTCCAGGGGGCCTGCC	ProLeuThrGluGluGluGluGluGluGlyAlaGlyAlaThrLeuSerArgGlyProAla	GGCCTGGACACCTGCAGAGCCTGGGACCACGTGGATGGGCAGATCCTGGGCCAACTGCGG	GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlvGlnLeuArg	GCCGGTGATGGTCCCACGCAGGAGGCGCTGTGGGACCCCGCTCTCTGGGCAGCCCTGTTCTTCTTA	AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu	ATGGGACCTAAAGACAGTGCCAAGTGCCTGCACCGTGGACCACAGCCGAGCCACTGGGCA	MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla
lyPhePheHisThrGlyHisGlnAsp 120 STTCTTCCACACAGGCCATCAGGAC 533	LaSerPheTyrAspTrpProLeuThr 100 	GGGCCACCTTGTCCAGGGGGCCTGCC 413			spGlyGlnIleLeuGlyGlnLeuArg 60				rgGlyProGlnProSerHisTrpAla 20

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13-NOV-2001;
08-FEB-2002;
08-FEB-2002;
12-APR-2002;
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Zlotnik
                              New genes that are up-regulated or down-regulated in cancers, markers for diagnosing e.g. cancer, ischemia or heart disease therapeutic targets for screening drugs for treating these di
Claim 8; Page 725-726; 767pp; English.
                                                                                                                                                                                                                                                                                                                                               17-SEP-2001;
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DB; ABR58693.
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; 2001US-0323887P.
; 2001US-0350687P.
; 2002US-0355145P.
; 2002US-0355257P.
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The present invention describes an isolated nucleic acid molecule, which CC comprises the sequence of any of the genes that are up-regulated or down-CC regulated in specific cancers (e.g. about 1031 genes up-regulated in CC acute lymphocytic leukemia). ACC72641 to ACC72880 represent cancer CC acute lymphocytic leukemia). ACC72641 to ACC72880 represent cancer CC absence of a pathological cell in a patient; (2) an expression vector CC absence of a pathological cell in a patient; (2) an expression vector CC comprising a nucleic acid molecule described above; (3) a host cell CC comprising the vector; (4) an isolated polypeptide, which is encoded by CC the nucleic acid; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a CC patient by administering to the patient the antibody above; and (7) a CC drug screening assay. The nucleic acid is useful as diagnostic markers or therapeutic targets. In particular, the nucleic acid is useful for the patient by administering to the patient the antibody above; and (7) a CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary, CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in CC capthologies.
pathologies
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Sequence 1268 BP; 204 A; 402 Ç 422 ç, 240 Ŧ, 0 U; 0 Other

No.:

3.64e-257 280.00 100.0% 100.0% 90.6%

Length:
Matches:
Conservative:
Mismatches:
Indels:

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181
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                  GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu
                                                                                                                                              TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg
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                The present invention relates to a DNA vaccine effective for eliciting an immune response against cancer cells which comprises a DNA construct operably encoding at least one cancer-associated Inhibitor of Apoptosis-family protein (IAP-family protein) and at least one immunoactive gene product in a pharmaceutical carrier. The invention is useful for treating cancer such as lung cancer, colorectal cancer and melanoma. The present sequence is the human livin beta splice variant DNA.
Sequence
                                                                                                                                                                                  WPI; 200
P-PSDB;
REFSEQ;
                                                                                                                Claim 26;
                                                                                                                                    New DNA vaccine comprising a cancer-associated Inhibitor of Apoptosis-family protein immunoactive gene product, useful for eliciting an immu response against cancer.
                                                                                                                                                                                                                              Xiang
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) REISFELD R !
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20-APR-2001 AAF24856; AAF24856

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel livin polypeptides and polynucleotides useful for treating pathophysiological disorders related to apoptosis, cancers, particularly melanoma cancer, Alzheimer's disease and Parkinson's disease e.g. by gen
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                                                                                                                                    GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg
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                             ProLeuThrGluGluGluGluGluGluGlyAlaGlyAlaThrLeuSerArgGlyProAla 80
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                                                17-OCT-2000; 2000JP-00316721.
20-DEC-2000; 2000JP-00386809.
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like polypeptides and encoded DNAs, applicable in diagnosis and screening
compounds for treating various cancers and apoptosis abnormality.
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                                                                                                                                        GACTTTGTCCACAGTGTGCAGGAGACTCACTCCCAGCTGCTGGGCTCYTGGGACCCGTGG
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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The invention relates to an antisense oligonucleotide targeted to a nucleic acid encoding Livin and that specifically hybridises with to nucleic acid encoding Livin and inhibits expression of Livin. The antisense oligonucleotide is useful for preparing a composition for
                                                                                                                                               New antisense oligonucleotide, having a sequence targeted to a nucleic acid encoding Livin, useful for preparing a composition for treating hyperproliferative disorder or aberrant apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-created the specific cancers (e.g. about 1031 genes up-regulated in caute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer caute lymphocytic leukemia. ACC72641 to ACC72860 represent cancer related gene nucleotide sequences which encode the proteins given in CC absence of a pathological cell in a patient; (2) an expression vector cc comprising a nucleic acid molecule described above; (3) a host cell comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a compound to a pathological cell in a cc drug screening assay. The nucleic acid is useful as diagnostic markers or comparising assay. The nucleic acid is useful as diagnostic markers or compound to a pathology, e.g. cancer (e.g. cancer of the bone marrow, cc diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases, cc drug screening, particularly for identifying agents for treating these cc pathologies
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20-SEP-2001; 2001US-0323887P.
13-NOV-2001; 2001US-0350666P.
08-FEB-2002; 2002US-0355145P.
08-FEB-2002; 2002US-035257P.
12-APR-2002; 2002US-0372246P.
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  New DNA vaccine comprising a family protein immunoactive
                                   WPI; 2004-689881/67.
P-PSDB; ADS71345.
REFSEQ; NM_139317.
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                                                                                                                                                                         24-MAR-2004; 2004US-00807897.
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                                                                                                         (REIS/)
                                                                                                                                                                                                                                                                                                                    Immune response; cancer-associated Inhibitor of Apoptosis-family protein; IAP-family protein; cancer; lung cancer; colorectal cancer; melanoma; human; livin alpha; gene; ds; immunostimulant; cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a human inhibitor of apoptosis protein, designated HIAP3. The protein is characterised by structural features common to the inhibitor of apoptosis protein family. The HIAP3 polypeptides can be used for the treatment of a disease state in a human patient, which is associated with inappropriate apoptosis and the patient is in need of increased levels of the polypeptide. Rhozymes, which target RNA encoding the polypeptide coding sequences, are useful for decreasing levels of the polypeptide for treatment of inappropriate apoptosis. Antisense nucleotide sequences are also useful for decreasing levels of the polypeptide. Regulation of inhibitor of apoptosis proteins may be useful in treatment of cancer, chronic viral infections, neurodegenerative disorders, chronic heart failure and dysfunctional
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11-FEB-1999;
22-APR-1999;
             Tang YT, 'Azimzai Y,
                                                                                                                                                                                                                                                                      Human; proliferation and apoptosis related protein; PROAP; psoriasis; cell proliferative disorder; immunological disorder; hepatitis; reproductive disorder; arteriosclerosis; cirrhosis; melanoma; lymphoma; cancer; acquired immune deficiency syndrome; AIDS; allergy; anaemia; asthma; diabetes mellitus; osteoarthritis; endometriosis; uterine fibroid; menstrual cycle; ss.
                                                                                                                                                   27-APR-2000
                                                                                                                                                                                                                                                                                                                                                   cDNA encoding a human proliferation and apoptosis related
                                               (INCY-)
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            Baughn
        H, Hillman JL, (
aughn MR, Yang J,
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99US-0118559P.
99US-0172229P.
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                                            PHARM
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         Guegler KJ,
, Shih LL;
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The present sequence encodes a human proliferation and apoptosis related protein (PROAP). The polypeptides and polynucleotides can be used for the diagnosis, treatment and prevention of cell proliferative, immunological and reproductive disorders. Disorders associated with decreased expression or activity of include arteriosclerosis, cirrhosis, hepatitis, psoriasis, melanoma, lymphoma and canneers of the breast, brain and prostate, acquired immune deficiency syndrome (AIDS), allergies, anaemia, asthma, diabetes mellitus, osteoarthritis, endometriosis, uterine fibroids and disruptions of the menstrual cycle. Antibodies against proap can be use in diagnosis of disorders characterized by PROAP e.g. in ELISA (enzyme linked immunosorbent assays) and the polynucleotides may be used to detect and quantify gene expression in biopsied tissues. These techniques can also be used to monitor regulation of PROAP levels during
                                           therapeutic intervention
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human proliferation and apoptosis related protein polypeptides for diagnosis, treatment and prevention of cell proliferative, immunological and reproductive disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Page 121; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-339688/29.
P-PSDB; AAY84907.
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Query DB: Alignment S Pred. No.: Percent Similarity:
Best Local Similarity:
Query Match: 5.1e-197 217.00 100.0% 100.0% 70.2% Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 1363 217 0 0 0

Sequence

BP;

228 A; 428

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Scores: 1363

US-09-762-577B-12 (1-309)x AAA15007

200	GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu ;	181	γΩ
754	GACTTTGTCCACAGTGTGCAGGAGACTCACTCCCAGCTGCTGGGCTCCTGGGACCCGTGG	695	ф
180	AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp	161	Ş
694	TGGACGGAGCATGCCAAGTGGTTCCCCAGCTGTCAGTTCCTGCTCCGGTCAAAAGGAAGA	635	Д
160	TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg	141	Q
634	AAGGTGAGGTGCTTCTTCTGCTATGGGGGCCTGCAGAGCTGGAAGCGCGGGGACGACCCC	575	뫄
140	LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro	121	8
574	GCTGAGGTGCCACCCGAGCTGCTGCTGCTGCCGGCTTCTTCCACACAGGCCATCAGGAC	515	DЬ
120	AlaGluValProProGluLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp	101	8
514	TTCCCCGGCATGGGCTCTGAGGAGTTGCGTCTGGCCTTCTTATGACTGGCCGCTGACT	455	당
100	PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr	81	Ş
454	CCCCTGACAGAGGAGGAAGAGGAGGAGGGCGCGGGGCCACCTTGTCCAGGGGGCCTGCC	395	뭥
80	ProLeuThrGluGluGluGluGluGluGlyAlaGlyAlaThrLeuSerArgGlyProAla	61	Ş
394	GGCCTGGACACCTGCAGAGCCTGGGACCACGTGGATGGGCAGATCCTGGGCCAGCTGCGG	335	Db
60	GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg	41	Ş
334	GCCGGTGATGGTCCCACGCAGGAGCGCTGTGGACCCCGCTTCTGGGCAGCCCTGTCCTA	275	Дb
40	AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu	21	Ş
274	ATGGGGCCTAAAGACAGTGCCAAGTGCCTGCACCGTGGACCACAGCCGAGCCAACTGGGCA	215	뮰
20	MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla	L	δ

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04-FEB-1999;
11-FEB-1999;
22-APR-1999;
19-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 200
P-PSDB;
                                                                     The present invention relates to the human proliferation and apoptosis related protein (PROAP) and its encoding nucleic acid. The invention is useful for diagnosing, preventing or treating disorders associated with altered expression or activity of human PROAP, such as cell proliferative (e.g. cancer or atherosclerosis), immunological (e.g. acquired immunodeficiency syndrome (AIDS) or allergies) or reproductive (e.g. infertility) disorders. The invention is also be used in screening for drugs that may be used for treating or preventing the disorders mentioned above and in gene therapy. The present sequence is the human PROAP-18
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Azimzai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROAP; proliferation and apoptosis related protein; cell proliferative disorder; cancer; atherosclerosis; immunological disorder; AIDS; acquired immunodeficiency syndrome; allergy; reproductive disorder; infertility; gene therapy; cytostatic; antiarteriosclerotic; immunosuppressive; anti-HIV; antiallergic; antiinfertility; gynaecological; human; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                             New human proliferation and apoptosis related proteins and polynucleotides for diagnosing, preventing or treating disorders associated with aberrant protein expression, e.g. cancer, AIDS, atherosclerosis or infertility.
                                                                                                                                                                                                                                                                                                                                              Claim 5;
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I, Baughn
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99WO-US024511.
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/product= "Proliferation
(PROAP)-18"
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Search completed: April 24, 2006, 11:11:43 Job time : 742 secs

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-Q-/abss/ABSSWEB_spool/US09762577/runat_24042006_105924_898/app_query.fasta_1
-DB=EST_QFWY=fastap_SUFFIX=p2noli.rst_-MINWATCH=0.1 -LOOPCL=0_-LOOPEXT=0
-UNITS=bits_START=1 -END=-1 -MATRIX=oligo_-TRANS=human40.cdi_-LIST-45
-DOCALIGN=200_-THR_SCORE=quality_-THR_MIN=1 -ALIGN=15 -MODE=LOCAL_OUTFWT=pto
-NORM=ext_-HEAPSIZE=500_-MINLEN=0_-MATRIX=0000000000_-TABS=02h
-USER=US09762577_@CGN_1_1_5315_@runat_24042006_105924_898_-NCPU=6_-ICPU=3
-NORM=PARN_TIMEOUT=30_-THREADS=1_-XGAPDE=60_-LONGLOG_-DEV_TIMEOUT=120
-WARN_TIMEOUT=30_-THREADS=1_-XGAPDE=60_-TGAPEXT=7
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BU180020 AGENCOURT
BQ892691 AGENCOURT
BU150825 AGENCOURT
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6	REFERENCE AUTHORS TITLE	RESULT 1 BU195879 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM		C 444444333333333333333333333333333333
Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM2328 row: o column: 12 High quality sequence stop: 658. Location/Qualifiers 1884	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 884) 1 (bases 1 to 884) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	884 bp mRNA linear 8050326 NIH_MGC_112 Homo sapiens cDNA clon sequence. GI:22709863 ns (human)	ALIGNMENTS	187 60.5 740 2 BG768992 BG768992 GO2742920 187 60.5 877 2 BG770075 BG778992 GO2742920 1885 59.9 956 5 BU168025

FEATURES source

/organism="Homo sapiens"

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RESULT 2
BQ682827
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GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCR0249 row: o column: 05
High quality sequence stop: 673.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Location/Qualifiers
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Tissue Procurement: DCTD/DTP
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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Hominidae; Homo.

1 (bases 1 to 621)
Wistow,G., Bernstein,S.L., Wyatt,M.K., Behal,A., Touchman,J.W.,
Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of adult human lens for the NEIBank
Project: over 2000 non-redundant transcripts, novel genes and
splice variants
Mol. Vis. 8 (4), 171-184 /^^^
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6/331, NIH, Bether Tel: 301 402 3452 Fax: 301 496 0078
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                                                                                                                                                              GluLeuArgLeuAlaSerPheTyrAspTrpProLeuThrAlaGluValProProGluLeu 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: graeme@helix.nih.gov
Plate: 04 row: c column:
TATGGGGGCCTGCAGAGCTGGAAGCGCGGGGACGACCCCTGGACGGAGCATGCCAAGTGG
                          TyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspProTrpThrGluHisAlaLysTrp 147
                                                                                           LeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAspLySValArgCysPhePheCys 127
                                                                                                                                       GAGTTGCGTCTGGCCTCCTTCTATGACTGGCCGCTGACTGCTGAGGTGCCACCCGAGCTG
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                                                                                                                                                                                                                                     GluGluGlyAlaGlyAlaThrLeuSerArgGlyProAlaPheProGlyMetGlySerGlu 87
                                                                                                                                                                                                                                                                                 TGGGACCACGTGGATGGGCAGATCCTGGGCCAGCTGCGGCCCCTGACAGAGGAGGAAGAG
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/note="Organ: Eye; Vector: pcMvSPORT6; A human lens
library (by) was normalized by self-subtraction. One
portion of double stranded plasmid DNA representing the
library was linearized by NotI. This NotI digested library
was used as a template for biotinylated RNA synthesis
using SP6 RNA polymerase. Another portion of the double
stranded plasmid library was converted to single-stranded
circles in vitro using Gene II and Exonuclease II (Life
Technologies). Single-stranded DNA (1 mg) was hybridized
(COt 500) with 41 mg of Bio-RNA and vector blocking
oligonucleotides. The hybridized Bio-RNA/ss-circles were
was performed on the library at the NIH Intramural
Sequencing Center(NISC)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wistow G
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/dev_stage="Adult"
/lab_host="EMDH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="fs04c01"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2402 row: d column: 12
High quality sequence start: 13
High quality sequence stop: 667.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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1 (Dases 1 to 945)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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5', mRNA sequence.
BU180020
BU180020.1 GI:22694004
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/clone lib="NIH MGC 112"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRIXhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript IRT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:6253787"
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Mismatches: Indels: Gaps:

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                                                                                                                                                                                                                                                                                                                                  929 bp mRNA linear EST 16-AUG-2002 AGENCOURT_8095843 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6087832 5', mRNA sequence.
found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM2325 row: a column: 17
                                       Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLN

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MCC clone distribution information
                                                                                                                                                    1 (bases 1 to 929)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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BQ892691.1 GI:22284705
EST.
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Location/Qualifiers
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 CTGCCCACACCC
                                                           GAAGAACCGGAAGACGCAGCCCCTGTGGCCCCCTCCCTGCCTCTGGGTACCCTGAG
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/note="Organ: skin, Vector: pOTB7; Site 1: XhoI, Site 2:
EcoRI; cDNA made by oligo-dT priming. DTrectionally clone into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6087832"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="melanotic melanoma, cell line"
/lab_host="DH108 (phage-resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
Plate: LLCM2501 row: a column: 19
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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AGENCOURT 8712345 NIH_MGC_112
5', mRNA fequence.
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Location/Qualifiers
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Tissue Procurement: DCTD/DTP
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                                                                                                  GluGluGluGluGlyAlaGlyAlaThrLeuSerArgGlyProAlaPheProGlyMet 84
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GGCTCTGAGGAGTTGCGTCTGGCCTCCTTCTATGACTGGCCGCTGACTGCTGAGGTGCCA
                          GlySerGluGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThrAlaGluValPro 104
                                                                                    GAGGAAGA
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                                                                                                                                                                                                                                CCCACGCAGGAGCGCTGTGGACCCCGCTCTCTGGGCAGCCCTGTCCTAGGCCTGGACACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="melanotic melanoma, cell line"
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/clone lib="NIH MGC_112"
/clone lib="NIH MGC_112"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5: adaptor:
GCCACGAC(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, laboratory of Gerald M. Rubin (University of California, Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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|mol_type="mRNA"
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100.0%
62.1%
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                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTp
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://imagg.llnl.gov
Plate: LLCM1749 row: g column: 06
High quality sequence stop: 740.
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1 (bases 1 to 740)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene
Unpublished (1999)
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/lab host="DH10B (phage-resistant)"
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/clone_lib="NH10B (phage-resistant)"
/clone_lib="NH1 MGC_49"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECGRI; CDNA made by oligo-dT priming. DTrectionally cToned
into ECGRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using_ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library. |"
                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
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                                                                                                                                                                                                                                                               /clone="IMAGE:4872605"
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                               Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC/DCTD/DTP
                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                            mRNA sequence. - - BG770075
BG770075.1 GI:14080728
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602745008F1 NIH_MGC_49 Homo sapiens
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                                                                                                         Hominidae; Homo.
                                                                                                                                                 Homo sapiens (human)
  cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (DNA Sequencing by: Incyte Genomics, Inc.
                                                                                                                                                                                                                                                       GluGluProGluAspAlaAla
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/tlissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_49"
/clone_lib="NIH_MGC_49"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI, CDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb_Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library. |"
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2327 row: n column: 03
High quality sequence start: 22
High quality sequence stop: 574.
Location/Qualifiers
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Tissue Procurement: DCTD/DTP
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NLH MGC_112"
/note="Organ: skin; Vector: pOTB7; Site_1: Xho1; Site_2:
EcoR1; CDNA made by oligo-dT priming. Directionally cloned
into EcoR1/Xho1 sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
BerKeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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164 HisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrpGluGluPro 183
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1 (bases 1 to 956)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM2356 row: i column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 535
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               /clone="IMAGE:6109915"
/tissue_type="melanotic melanoma, cell line"
/tissue_type="melanotic"
/tisue_t
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                   1 (bases 1 to 958)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                      958 bp
AGENCOURT 7962186 NIH MGC_112 Homo
5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                GCCGGTGATGGTCCCACGCAGGAGCGCTGTGGACCCCGCTCTCTGGGCAGCCCTGTCCTA
     Glu 181
                                                                                                                                          LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro
                                                                                                                                                                                                                                                                              CCCCTGACAGAGGAGGAAGAGGAGGAGGCCCGGGGCCACCTTGTCCAGGGGGCCTGCC
                            GACTTTGTCCACAGTGTGCAAGAGACTCACTCCCAGCTGCTGGGCTCCTGGGACCCGTGG
                                                                                            TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg
                                                                                                                                                                                                                                                                                             ProLeuThrGluGluGluGluGluGlyAlaGlyAlaThrLeuSerArgGlyProAla
                                                                                                                                                                                                                                                                                                                                              GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg
                                           AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp
                                                                           TGGACGGAGCATGCCAAGTGGTTCCCCCAGCTGTCAGTTCCTGCTCCGGTCAAAAGGAAGA
                                                                                                                                                                             PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr
                                                                                                                                                                                                                                                                                                                                GGCCTGGACACCTGCAGAGCCTGGGACCACGTGGATGGGCAGATCCTGGGCCAGCTGCGG
                                                                                                                                                                                                                                                                                                                                                                                               AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu
                                                                                                                                                                                                                              TTCCCCGGCATGGGCTCTGAGGAGTTGCGTCTGGCCTCCTTCTATGACTGGCCGCTGACT
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Indels:
Gaps:
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Matches:
Conservative:
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564

624

120

504 100 444 80 384 60 324 40 264 20

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DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov http://image.llnl.gov c column: 07 High quality sequence start: 12 High quality sequence stop: 611.
/mol type="mRNA"
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/clone="IMAGE:6106302"
/tissue_type="melanotic melanoma, cell line"
/tissue_type="melanotic melanoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_112"
/clone_l
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US-09-762-577B-12 (1-309) x BM696272 (1-603)
                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                     Pred. No.:
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BM696272
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Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: Dr. Gregg Hageman cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM696272 603 bp mRNA linear EST 28-FEB-2002 UI-E-DW0-agl-c-11-0-UI.r1 UI-E-DW0 Homo sapiens cDNA clone UI-E-DW0-agl-c-11-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Normalization and subtraction:
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Bonaldo, M.F., Lenno
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Mammalia; Eutheria;
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                                                                                                                                                               /note-Dryan: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-DWO is a cDNA library containing the following tissue(s): lens. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The first-strand cDNA contains a library tag sequence that is sequence tag for this library is CASTTACCA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="UI-E-DW0-ag1-c-11-0-UI"
/tissue_type="lens"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type≈"mRNA"
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                                     2.45e-162
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and subtraction: two approaches to
                                                                                                                                                                                                                                                                                                                                                                                                                       host="DH10B (Life Technologies) (T1 phage resistant)"
e_lib="UI-E-DW0"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
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161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp
                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2331 row: e column: 07
High quality sequence stop: 580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 GGCCTGGACACCTGCAGAGCCTGGGACCACGTGGATGGGCAGATCCTGGGCCAGCTGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae; Homo.

1 (bases 1 to 870)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
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EST.
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AGENCOURT_8042576 NIH_MGC_112

5', mRNA secrience.
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                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bp
2 Homo
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sapiens cDNA clone IMAGE:6090222
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Percent Similarity:
Best Local Similarity:
Query Match:

2.44e-158 176.00 100.0% 100.0% 57.0%

Pred. No.: Alignment ORIGIN

US-09-762-577B-12 (1-309) x BQ877438 (1-870)

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1 (bases 1 to 912)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySer
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
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                                                                  TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg
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AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySer 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:6263255"
/tlissue_type="melanotic melanoma, cell line"
/tissue_type="melanotic melanoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 112"
/clone lib="NIH MGC 112"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
/note="Organ: skin; Vector: pOTB7; Site 1: Adaptor:
EcoRJ(XhoI sites using the following 5: adaptor:
into EcoRJ(XhoI sites using the following 5: adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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100.0%
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57.0%
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REFERENCE AUTHORS TITLE JOURNAL

RESULT 15 BQ682378 LOCUS

DEFINITION

912)
AGENCOURT 8185884 NIH MGC 112
5', mRNA sequence.
ROGE2270

bp 2 Homo

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141

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124

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ACCESSION VERSION

BQ682378 BQ682378.1 EST.

GI:21795057

KEYWORDS

SOURCE ORGANISM

Homo sapiens Homo sapiens (human)

Hominidae; Homo.

Db 544 GACTTTGTCCACAGTGTGCAGGAGACTCACTCCCAGCTGCTGGGCTCC 591
Search completed: April 24, 2006, 11:15:00
Job time : 4516 secs

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Command line parameters:

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-Q-|abbss/ABSSWEB_spool/US09762577/runat_24042006_105928_1006/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap_-SUPFIX=p2nol1.rni -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE-quality -THR MIN=1 -ALIGN=15 -MODE-LOCAL
-UTFMT=pto -NORM-ext -HBAPSIZE=500 -MINLEN-0 -MAXIEN=2000000000 -HOST=abss06h
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-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -TGAPEDF=60 -FGAPEXT=7
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and is derived
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8: /cgn2_6/ptodata/l/ina/RE_COMB.seq:*

9: /cgn2_6/ptodata/l/ina/RE_COMB.seq:*
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Match Length
                                                                                                                                                                                                                                                                                                                                                             is the number of results predicted by chance to have a ster than or equal to the score of the result being printed,
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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d by analysis of the total score distribution.
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US-09-127-928-1

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US-09-949-016-66140

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US-09-016-66134
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Sequence 1949, Ap
Sequence 1, Appli
Sequence 13691, A
Sequence 66130, A
Sequence 66140, A
Sequence 66139, A
Sequence 334, App
Sequence 66134, A
Sequence 216, App
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W	w	N	σ	w	w	w	Φ	w	w	w	σ	w	w	ω	W	ω	w	ω	N	w	w	w	w	w	w	w	σ	w	w	w	ω	w	w	W	ω
2-	9-814-	-09-205-1	US96-12860	10-232-286-1	-09-689-36	8-569-749-1	-12860-	0-232-286-	-09-689-3	08-569-749-	T-US96-12860	-10-232-28	-09-689-366-	-08-569-749-	-09-201-9	-09-67	-09-011-35	US-09-201-936-7	-08-511-	US-09-023-655-894	-09-016-434-1	-09-201-932-	-09-672-717-2	-09-011-356-4	-09-201-936-4	9-023-655-49	T-US95-05	-09-949-016-176	US-09-949-016-21029	-09-949-016-661	-09-949-016-6613	-09-949-016-6613	-09-949-016-661	-09-949-016-6613	9-023-655-3
equence 13,	e 11,	equence 1	equence 13,	e 13,	Sequence 13, Appl	equence 13,	e 3, A	equence 3, App	e 3, A	3, App	<u>, , , , , , , , , , , , , , , , , , , </u>	1,	e 1,	e 1,	e 7, Appl	e 222, Ap	e 7,	e 7,	e 7, Appl	e 894, <i>1</i>	e 1076	e 41, App	e 228,	e 41,	e 41, App	e 497,	e 1, Ap	e 17607	e 210	e 66137,	e 661	e 6613	e 6613	e 66138,	87, Ap

ALIGNMENTS

RESULT 1 US-09-949-016-1949

Sequence 1949, Appropriate Patent No. 681233

Application US/09949016

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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PELLING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE
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Sequence 1, Application US/09127928
Patent No. 6472172
Patent No. 6472172
Patent No. 6472172
Patent INFORMATION:
APPLICANT: Deng, Gang
APPLICANT: Lin, Jiing-Huey
APPLICANT: Morser, Michael J
TITLE OF INVENTION: DNA Encoding a No. 64721
TITLE OF INVENTION: Protein
FILE REFERENCE: DNA Encoding HIAP3
CURRENT APPLICATION NUMBER: US/09/127,928
CURRENT FILING DATE: 1998-07-31
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
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US-09-949-016-13691 Application US/09949016

Sequence 13691 Application US/09949016

Patent NO. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITHORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016
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; LENGTH: 1337
; TYPE: DNA
; ORGANISM: Homo sap:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (170)...(:
US-09-127-928-1
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Best Local Similarity:
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Gaps:
                                                                 ASSOCIATED OF DETECTION
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                                                              USES THEREOF
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RESULT 2 US-09-127-928-1

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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CLOOL307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-327,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-337,768
PRIOR FILING DATE: 2000-09-08
VOUNBER OF SEQ ID NOS: 207012
SOFTWARE: FASCUSQ for Windows Version 4.0
SEQ ID NO 66130
LENGTH: 601
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Best Local Similarity:
Query Match:
DB:
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US-09-949-016-66130
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; ORGANISM: Human
US-09-949-016-13691
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 13691
                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         Sequence 66130, Application US/09949016 Patent No. 6812339
TYPE: DNA
ORGANISM: Human
-09-949-016-66130
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66140
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILLING DATE: 2000-10-03
PRIOR FILLING DATE: 2000-10-03
PRIOR FILLING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SECTIMARE: FastSEQ for Windows Version 4.0
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 66140, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 66140
547
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                GluCysAlaProGlyLeuGlnLeuCysProIleCysArgAlaProValArgSer 273
                                                                           ValCysLeuAspArgAlaValSerIleValPheValProCysGlyHisLeuValCysAla
                                                                                                                        CCAGGAGCCAGGGATGTGGAGGCGCAGCTGCGGCGGCTGCAGGAGGAGGACGTGCAAG
                                                                                                                                       ProGlyAlaArgAspValGluAlaGlnLeuArgArgLeuGlnGluGluArgThrCysLys
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Matches:
Conservative:
Mismatches:
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Matches:
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-08

NUMBER OF SEQ ID NOS: 207012
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FO
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ANDRESSES
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US-09-949-016-66139
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 334, Application US/09023655
Patent No. 6607879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 66139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 66139, App
Patent No. 6812339
        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 601
                                                                                                                                                           COUNTRY: USA
      APPLICATION NUMBER:
                                                                                                                                                                                                   STREET: 3174 PORTER DRIVE CITY: PALO ALTO
                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          575 GAGTGTGCCCCCGGCCTGCAGCTGTGC 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 ValCysLeuAspArgAlaValSerIleValPheValProCysGlyHisLeuValCysAla 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         455 CCAGGAGCCAGGGATGTGGAGGCGCAGCTGCGGCGGCTGCAGGAGGAGGAGGACGTGCAAG
                                                                                                                                           94304
                                                                                                                                                                                CALIFORNIA
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US/09/023,655
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Matches:
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Indels:
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Alignment Scores: Pred. No.:
                                                 ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66134
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Best Local Similarity:
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                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 66134
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                                                                                                                                                      APPLICANTION UNMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 66134, Application US/09949016 Patent No. 6812339 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION UNMBER: PA-0
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                     LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (650) 845-4166 INFORMATION FOR SEQ ID NO: :
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LIBRARY: KIDNNOT09
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1419118
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TYPE: nucleic acid
STRANDEDNESS: single
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Matches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-016-434-216
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US-09-762-577B-12 (1-309) x US-09-016-434-216 (1-200)
                                                          Percent Similarity:
Best Local Similarity:
                                                                                                           Alignment Scores:
Pred. No.:
                                                Query Match:
                                                                                                                                                        US-09-016-434-216
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Patent No. 6500938
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                                                                                                                                                                                                                                                                                            TELEFAX: (650) 845-410
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
                                                                                                                                                                                                    IMMEDIATE SOURCE:
                                                                                                                                                            LIBRARY: BLALLINE: 1520835
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                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                STRANDEDNESS: single
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, NO: 216:
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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                                                                                                                                             Query Match:
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US-09-023-655-387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cocks, Benjamin G. APPLICANT: Susan G. Stuart APPLICANT: Jeffrey J. Seilhamer TITLE OF INVENTION: COMPOSITION TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
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APPLICATION NUMBER: US
FILING DATE: HEREWITH
CLASSIFICATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                              No.:
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CITY: PALO ALTO
STATE: CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                         LENGTH: 200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
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                                                   226 ArgArgLeuGlnGluGluArgThrCysLysValCysLeuAspArgAlaValSerIleVal
246 PheValProCysGlyHisLeuValCysAla 255
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                               40 CGGCGGCTGCAGGAGGAGGACGTGCAAGGTGTGCCTGGACCGCGCCGTGTCCATCGTC
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Matches:
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Indels:
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PATENT APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
   Alignment Scores: Pred. No.:
                                                  ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66135
                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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US-09-949-016-66135
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DB:
                                                                                              NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 66135
LENGTH: 601
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Best Local Similarity:
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US-09-949-016-66138
                                                                                                                                                                                                                                                                                           Sequence 66135, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001307
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 66138
LENGTH: 601
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; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66136
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Query Match:
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                                          Sequence 66131, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TIFLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TIFLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
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US-09-949-016-66136
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Best Local Similarity:
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001197

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 60/231,498

PRIOR FILING DATE: 2000-10-08

PRIOR FILING DATE: 2000-09-08
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Patent No. 6812339
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                    221 AGCTGTCAGTTCCTGCTCCGGTCAAAAGGAAGAGACTTTGTCCACAGTGTGCAGGAGACT
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US-09-949-016-66137
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; ORGANISM: Human
US-09-949-016-66131
                                                                                                                                                                                                                          Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                   ; NUMBER OF SEQ ID NOS: 207012
; SCPTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 66137
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66137
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                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-010-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
RUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 66131
LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 66137, Application US/09949016 Patent No. 6812339
409
                            213
                                                       91 LeuAlaSerPheTyrAspTrpProLeuThrAlaGluValProProGluLeuLeuAlaAla 110
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                 AlaGlnGluProGlyAla 218
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GCCCAGGAGCCAGGTGCA 426
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Search completed: April 24, 2006, 10:02:44
Job time: 166 secs

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-DB=Published_Applications_NA_Main -QFWT=fastap -SUFFIX=p2noli.rnpbm
-NINMATCH=0.1 -LOOPEL-0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR_MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-USER=US09762577_GCGN_1 1 797 @runat 24042006 105937_1201 -NCPU=6 -ICPU=3
-NO_MAAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THRANDS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
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1: /cgm2 6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgm2 6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

3: /cgm2 6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

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5: /cgm2 6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

6: /cgm2 6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

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8: /cgm2 6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

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Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-188-646-4

US-10-807-897-28

US-10-244-586-1

US-10-188-646-12

US-10-188-646-12

US-10-807-897-26-1
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Sequence 17, Appli
Sequence 26, Appli
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equence 228, Ap	quence 47, App	equence 49	equence	equence 1,	equence 58	equence 80	e 20	e 20	equence 14525	e 14525	Φ	equence 14525	equence 14525	equence 14525	equence 14509	equence 14509	quence 14214	equence 14213	equence 14214	equence 1421	equence 27355	equence 387,	e 216,	equence 334,	equence 1236	equence 4448,	e 1, App	equence 27357,	e 11	equence 63, Ap	e 27354,	equence 8265,	e 22, Ap	equence	equence 21, Ap	7, Aç

ALIGNMENTS

RESULT 1 US-10-244-586-2

Sequence 2, Application US/10244586 Publication No. US20030087319A1

GENERAL INFORMATION:

APPLICANT: GOMES, BRUCE C.

APPLICANT: KASOF, GARRETT M.

APPLICANT: PROSSER, JUDITH C.

TITLE OF INVENTION: NOVEL PROTEIN

FILE REFERENCE: DJB/009901/0270799

CURRENT APPLICATION NUMBER: US/10/244,586

CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: US/09/594,119

PRIOR FILING DATE: 2000-06-14

PRIOR APPLICATION NUMBER: 60/139,291

PRIOR PILING DATE: 1999-06-15

NUMBER OF SEQ ID NOS: 12

SEC IN NO.

SEQ ID NO 2

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; LENGTH: 843
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-244-586-2
Alignment Scores: 2.67e-273 Length: 843
Pred. No.: 280.00 Matches: 280
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Ouery Match: 90.6% Indels: 0
DB: Gaps: 0
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RESULT 2
US-10-188-646-4
Sequence 4, Application US/10188646
Publication No. US20040005565A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF
FILE REFERENCE: RTS-0373
CURRENT APPLICATION NUMBER: US/10/188,646
CURRENT APPLICATION DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 153
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Sequence 28, Application US/10807897
Publication No. US20040192631A1

GENERAL INFORMATION:
APPLICANT: Xiang, Rong
APPLICANT: Zhou, He
APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: DNA VACCINES AGAINGT TUMOR
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: TSRI-874.1
CURRENT FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: US/10/807,897
PRIOR APPLICATION NUMBER: 60/457,009
PRIOR FILING DATE: 2003-03-24
PRIOR FILING DATE: 2003-03-24
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; LOCATION: (174)...(1016)
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SEQ ID NO 28
LENGTH: 1268
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ORGANISM: homo
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Sequence 1, Application US/10244586
Publication No. US20030087319A1
GENERAL INFORMATION:
APPLICANT: GOMES, BRUCE C.
APPLICANT: KASOF, GARRETT M.
APPLICANT: PROSSER, JUDITH C.
TITLE OF INVENTION: NOVEL PROTEIN
FILE REFERENCE: DJB/009901/0270799
CURRENT APPLICATION NUMBER: US/10/244,586
CURRENT FILING DATE: 2002-09-16
CURRENT FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US/09/594,119
RRIOR FILING DATE: 1999-06-15
PRIOR FILING DATE: 1999-06-15
PRIOR FILING DATE: 1999-06-15
SOFTWARE: Patentin Ver: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1376
TYPE: DNA
ORGANISM: Homo sapiens
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                                                ProLeuThrGluGluGluGluGluGluGluGlyAlaGlyAlaThrLeuSerArgGlyProAla
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; FEATURE:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1).
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Pred. No.:
                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                               US-09-762-577B-12 (1-309)
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US-10-188-646-12
i Sequence 12, Application US/10188646
publication No. US20040005565A1
GENERAL INFORMATION:
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APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
FILE REFERENCE: RTS-0373
CURRENT APPLICATION NUMBER: US/10/188,646
CURRENT FILING DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 12
LENGTH: 1168
TYPE: DNA
ORGANISM: H. sapiens
                                                                                                                                    Scores:
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Matches:
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APPLICANT: Xiang, Rong
APPLICANT: Xiang, Rong
APPLICANT: Reisfeld, Ralph A.
APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GRO
TITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GRO
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: TSRI-874.1
CURRENT APPLICATION NUMBER: US/10/807,897
CURRENT FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/457,009
PRIOR FILING DATE: 2003-03-24
NUMBER OF SEQ ID NOS: 29
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 1322
TYPE: DNA
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (174)...(1070)
US-10-807-897-26
                                        Alignment s
Pred. No.:
Score:
 Percent Similarity:
Best Local Similarity:
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US-10-807-897-26
; Sequence 26, Application US/10807897
; Publication No. US20040192631A1
; GENERAL INFORMATION:
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Conservative:
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RESULT 7
US-10-235-026-1
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                                                                                                                                                      Sequence 1, Application US/10235026

Publication No. US20030082725A1

GENERAL INFORMATION:
APPLICANT: Lin, Jiing-Huey
APPLICANT: Lin, Jiing-Huey
APPLICANT: Morser, Michael J
TITLE OF INVENTION: DNA Encoding a No. US20030082725A1el Human Inhibitor-of-Apoptosis
FILE REFERENCE: 50972AUSD1
CURRENT APPLICATION NUMBER: US/10/235,026
CURRENT FILING DATE: 1098-07-03
PRIOR APPLICATION NUMBER: US 09/127,928
PRIOR FILING DATE: 1998-07-31
NUMBER OF SEQ ID NOS: 7
COCCURRENT FILING DATE: 1998-07-31
NUMBER OF SEQ ID NOS: 7
                                                                                                           SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1337
                                                            TYPE: DNA
ORGANISM: Homo
FEATURE:
            NAME/KEY: CDS
LOCATION: (170)..(1066)
OTHER INFORMATION:
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US-10-839-882-37
US-10-839-882-37
Sequence 37, Application US/10839882
Publication No. US20040203106A1
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Best Local Similarity:
Query Match:
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                                                     APPLICANT: INCYTE PHARMACEUTICALS, I
APPLICANT: TANG, Y. TOM
APPLICANT: YUE, Henry
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: GUEGLER, Karl J.
APPLICANT: CORLEY, Neil C.
APPLICANT: LAL, Preeti
APPLICANT: AZIMZAI, Yalda
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BAUGHN, Mariah R.
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        APPLICANT:
APPLICANT:
TITLE OF IN
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CANT: TANG, Y. Tom
CANT: YUE, Henry
CANT: HILLMAN, Jennifer L.
CANT: GUEGLER, Karl J.
CANT: CORLEY, Neil C.
CANT: LAL, Preeti
CANT: AZIMZAI, Yalda
CANT: BAUGHN, Mariah R.
CANT: BAUGHN, Mariah R.
CANT: SUMNING, Yang
CANT: SHIH, Leo L.
OF INVENTION: PROLIFERATION AND APOPTOSIS RELATED PROTEINS
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Matches:
Conservative:
Mismatches:
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DB:
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Best Local Similarity:
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Pred. No.:
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SEQ ID NO 37
LENGTH: 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 44
SOFTWARE: PERL Program
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PRIOR FILING DATE: 1998-10-20; 1998-10-20; 1999-02-04; 1999-04-11; 1999-04-11; 1999-04-11; 1999-04-11; 1999-04-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: PF-0619 PCT
CURRENT APPLICATION NUMBER: US/10/839,882
CURRENT FILING DATE: 2004-05-05
PRIOR APPLICATION NUMBER: US/09/807,452
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/175,737; unassigned; 60/118,559; 09/249,740; unassigned;
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID
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; TYPE: DNA
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US-10-203-708-21
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CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR FILING DATE: 2001-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 60/186,084
PRIOR FILING DATE: 2000-02-29
NUMBER: OF SEQ ID NOS: 46
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US-10-203-708-21
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Publication No. US20030149238A1
GRMERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM P.1.C.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50013
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GACTTTGTCCACAGTGTGCAGGAGACTCACTCCCAGCTGCTGGGCTCCTGG
                      AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrp
                                                                   TGGACGGAGCATGCCAAGTGGTTCCCCCAGCTGTCAGTTCCTGCTCCGGTCAAAAGGAAGA
                                                                                             TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg
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US-10-723-860-4697
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Sequence 4697, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
Sequence 22, Application US/10203708
Publication No. US20030149238A1
GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM P.1.C.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50013
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APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
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Sequence 8265, Application US/10723860
Publication No. US20040253608A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Glotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of S;
TITLE OF INVENTION: Methods for Screening fo
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
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US-10-723-860-8265
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; ORGANISM: Homo
US-10-203-708-22
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CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 60/186,084
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
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LENGTH: 769
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NUMBER OF SEQ ID NOS: 8393

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APPLICANT: Hyseq, Inc
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CLF3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILLING DATE: 2001-03-30
PRIOR FILLING DATE: 2000-03-31
PRIOR FILLING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILLING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUstom
SSEQ ID NO 27354
LENGTH. 614
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Best Local Similarity:
Query Match:
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; ORGANISM: Homo
US-10-723-860-8265
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SOFTWARE: Pater
SEQ ID NO 8265
FUNGTH: 858
                                                                                                                                                                                                                                                                                                                                                   Sequence 27354, Application US/10450763 Publication No. US20050196754A1 GENERAL INFORMATION:
NAME/KEY: SIMILAR
LOCATION: (309)..(614)
COTHER INFORMATION: 35% homologous to Homo sapiens inhibitor of apoptosis protein
OTHER INFORMATION: KIAP, accession number AF301009, Smith-Waterman Score=86.
                                                                           LENGTH: 614
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity:
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-296-115-63
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TITLE OF INVENTION: NO. US20040053248A1el Nucleic Acids and Polypeptides
FILE REFERENCE: 784PCT
CURRENT APPLICATION NUMBER: US/10/296,115
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION UNUMER: US09/488,725
PRIOR APPLICATION UNUMER: US09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION UNMER: US09/552,317
PRIOR APPLICATION UNMER: US09/552,317
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 1478
**PRIOR FILING DATE: 2000-04-25
UNMBER OF SEQ ID NOS: 1478
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Publication No. US20040053248A1
GENERAL INFORMATION:
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RESULT 15

US-10-188-646-11

US-10-188-646-11

Sequence 11, Application US/10188646

Publication No. US20040005565A1

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION

FILE REFERENCE: RTS-0373

CURRENT APPLICATION NUMBER: US/10/188,646

CURRENT FILING DATE: 2002-07-02

NUMBER OF SEQ ID NOS: 153

SEQ ID NO 11

LENGTH: 4810

TYPE: DNA

ORGANISM: H. sapiens
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PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
                                                                                                                             ProLeuThrGluGluGluGluGluGlyAlaGlyAlaThrLeuSerArgGlyProAla 80
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Search completed: April 24, 2006, 10:13:42

Job time : 631 secs

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Result
No.
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 177
149
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Match Length DB ID
57.3
48.2
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769
14
14
US-11-135-855-21
US-11-135-855-22
                    Description
Sequence 21,
Sequence 22,
App1
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-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
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2: /SIDS5/ptodata/2/pubpna/USO7_NEW_PUB.seq:*

3: /SIDS5/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

4: /SIDS5/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

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| SIDSS/ptodata/2/pubpna/US10_NEW_PUB_seq: *
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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PRIOR APPLICATION NUMBER: US/10/203,708
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 60/186,084
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FRACESEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 1068
TYPE: DNA
ORGANISM: Homo sapiens
US-11-135-855-21
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US-11-135-855-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/11135855 Publication No. US20050255557A1
                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: GP50013
CURRENT APPLICATION NUMBER: US/11/135,855
CURRENT FILING DATE: 2005-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SMITHKLINE BEECHAM CORPORATION APPLICANT: SMITHKLINE BEECHAM p.l.c.
TITLE OF INVENTION: NOVEL COMPOUNDS
                                                                                                                                                         FastSEQ for Windows Version 3.0
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APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM p.l.c.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50013
CURRENT FILING DATE: 2005-05-24
PRIOR APPLICATION NUMBER: US/10/203,708
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR APPLICATION NUMBER: 60/186,084
PRIOR APPLICATION NUMBER: 60/186,084
PRIOR FILING DATE: 2000-02-29
SUMBER OF SEQ ID NOS: 46
SOPTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 22
LENGTH: 769
TYPE: DNA
ORGANISM: HOW Sapiens
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US-11-135-855-22
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Best Local Similarity:
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Pred. No.:
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Publication No. US20050255557A1
GENERAL INFORMATION:
-11-135-855-22
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RESULT 3
US-10-960-414-432
; Sequence 432, Applicat
; Publication No. US2006
; GENERAL INFORMATION:
                                                                                                                                           APPLICANT: MILLER, LANCE D.

APPLICANT: GEORGE, JOSHY

APPLICANT: GEORGE, JOSHY

APPLICANT: UEGA, VINSENSIUS B.

TITLE OF INVENTION: METHODS, SYSTEMS, AND COMPOSITIONS FOR CLASSIFICATION,

TITLE OF INVENTION: PROGNOSIS, AND DIAGNOSIS OF CANCERS

FILE REFERENCE: 38271-76067

CURRENT APPLICATION UNMUBER: US/10/960,414

CURRENT FILING DATE: 2004-10-06

NUMBER OF SEQ ID NOS: 500

SOFTWARE: Patentin version 3.3

SEQ ID NO 432

LENGTH: 3076

TYPE: DNA

ORGANISM: Homo sapiens
                                                        Percent Similarity:
Best Local Similarity:
    US-09-762-577B-12 (1-309)
                                               Query Match:
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APPLICANT: Wyeth
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT ELIUNG DATE: 2005-05-25
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 2596
LENGTH: 3837
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APPLICANT: Wounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6853
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                                                                                                                                                             TYPE: DNA ORGANISM: Rattus norvegicus
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LOCATION: (3829) . (3831)
OTHER INFORMATION: n is
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ORGANISM: Rattus norvegicus
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Percent Similarity:
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Best Local Similarity:
Query Match:
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Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILLE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR APPLICATION DATE: 2002-08-09
PRIOR APPLICATION DATE: 2002-08-09
                     Query Match:
                                                                                     Score:
                                                                                                                          Alignment Scores:
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US-10-301-480-653234
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PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 39825
LENGTH: 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 653234, Application US/10301480 Publication No. US20060057564A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                     SEQ ID NO 653234
                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, David G.

TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR APPLICATION NUMBER: US 06/311,695
PRIOR PILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
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SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: DNA
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US-09-762-577B-12 (1-309) x US-11-136-527-303 (1-2468)
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Best Local Similarity:
Query Match:
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US-11-136-527-303
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Best Local Similarity:
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US-11-136-527-2757
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APPLICANT: Weth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOCTWARE: Patentin version 3.2
SEQ ID NO 303
LENGTH: 2468
TYPE: DNA
TYPE: DNA
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APPLICANT: Wyeth
APPLICANT: Mounts, William M
ITILE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR APPLICATION NUMBER: US 60/574,294
OF THE PRIOR APPLICATION OF SECONDAME: PRIOR FILING DATE: 2005-05-26
NUMBER OF SECONDAME: PATENTIAL PATENTAL PATENT
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TITLE OF INVENTION: GENETIC POLYMORPHISMS AS TITLE OF INVENTION: CARDIOVASCULAR DISORDER TITLE OF INVENTION: DETECTION AND USES THEF FILE REFERENCE: CL001559
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 63908
                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
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 RESULT
                                                                                              US-09-762-577B-12 (1-309)
                                                                                                                                                                                                                               Alignment Scores:
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US-10-995-561-64173/c
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS:
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILLING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 64173
LENGTH: 201
TYPE: DNA.
GEORGISM. WORDS.
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Publication No. US20050272054A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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GENETIC POLYMORPHISMS ASSOCIATED WITH
CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
DETECTION AND USES THEREOF
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CURRENT APPLICATION NUMBER: US/11/128,061
CURRENT FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: Pateentin version 3.3
SEQ ID NO 5527
LENGTH: 599
TYPE: DNA
CORGANISM: Cricetulus griseus
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CURRENT FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1885
LENGTH: 599
TYPE: DNA
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US-11-128-061-5527
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sinacore, Martin S.
APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
FILE REFERENCE: 01997.027701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sinacore, Martin S.
APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Melville, Mark W. APPLICANT: Charlebois, Timo APPLICANT: Mounts, William | APPLICANT: Hann, Louane E.
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APPLICANT: Charlebois, Timo
APPLICANT: Mounts, William
APPLICANT: Hann, Louane E.
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NAME/KEY: misc_feature
LOCATION: (26)..(71)
NAME/KEY: misc_feature
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Mounts, William M.
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US-11-128-049-5527
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Best Local Similarity:
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; OTHER INFORMATION: n is a,
US-11-128-061-5527
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Sequence 5527, Application US/11128049 Publication No. US20060010513A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.3 SEQ ID NO 1885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1885, Application US/11128049 Publication No. US20060010513A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/11/128,049
CURRENT FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS
TITLE OF INVENTION: MAKING AND USING SAME
FILE REFERENCE: 01997.027700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Melville, Mark W.
APPLICANT: Charlebois, Timothy
APPLICANT: Mounts, William M.
APPLICANT: Hann, Louane E.
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NAME/KEY: misc_feature
LOCATION: (26)..(71)
OTHER INFORMATION: n is a,
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TYPE: DNA
ORGANISM: Cricetulus griseus
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Leonard, Mark W.
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Matches:
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Mismatches:
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GENERAL INFORMATION:
APPLICANT: Melville, Mark W.

APPLICANT:
APPLICANT:

Charlebois, Timor...,
Mounts, William M.
Touane E.

Timothy S

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APPLICANT: Sinacore, Markin S.
APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: OLIGONUCLECTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR TITLE OF INVENTION: MAKING AND USING SAME
FILE REPERENCE: 0.1997.027700
CURRENT APPLICATION NUMBER: US/11/128,049
CURRENT APPLICATION NUMBER: US/570,425
PRIOR FILING DATE: 2004-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
INUMBER OF SEQ ID NOS: 7285
SOCTWARE: Patentin version 3.3
SEQ ID NO 5527
LENGTH: 599
TYPE: DNA
ORGANISM: Cricetulus griseus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (26)..(71)
OTHER INFORMATION: n is a, c, g, or t
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Best Local Similarity:
Query Match:
DB:
Search completed: April 24, 2006, 10:45:06 Job time : 1858 secs
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-ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
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Fgapop 60.0,
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                          US-09-762-577B-12
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/ Cgn2_6/ptodata/1/pna/US06_COMB.seq:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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PCT-US99-17738-11 PCT-US93-20821-4 US-10-170-235-27143 US-10-188-646-4 US-10-553-355-11	27 US-09-594-119-2 43 US-10-244-586-2	ID
Sequence 11, Appl Sequence 4, Appli Sequence 27143, A Sequence 4, Appli Sequence 11, Appl	Sequence 2, Appli Sequence 2, Appli	Description

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Sequence 2, Application US/09594119
GENERAL INFORMATION:
APPLICANT: GOMES, BRUCE C.
APPLICANT: KASOF, GARRETT M.
APPLICANT: PROSSER, JUDITH C.
TITLE OF INVENTION: NOVEL PROTEIN
FILE REFERENCE: DIB/009901/0270799
CURRENT APPLICATION NUMBER: US/09/594,119
CURRENT FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: 60/139,291
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
LENGTH: 843
TYPE: DNA
ORGANISM: Homo sapiens
US-09-594-119-2
                                                                                                                                                                                            Alignment & Pred. No.:
                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                      US-09-762-577B-12 (1-309) x US-09-594-119-2 (1-843)
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16 US-10-940-774A-1949
17 US-10-940-774A-1949
18 PCT-US02-29560A-182
19 PCT-US02-29560A-182
19 PCT-US02-29560A-182
20 US-10-807-897-28
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21 US-10-244-586-1
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Sequence 1949, Ap
Sequence 182, App
RESULT 2
US-10-244-586-2
US-10-244-586-2
; Sequence 2, Application US/10244586
; GENERAL INFORMATION:
; APPLICANT: COMES, BRUCE C.
; APPLICANT: PROSSER, JUDITH C.
; APPLICANT: PROSSER, JUDITH C.
; TITLE OF INVENTION: NOVEL PROTEIN
; FILE REFERENCE: DJB/009901/0270799
; CURRENT APPLICATION NUMBER: US/10/244,586
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US/9/594,119
; PRIOR APPLICATION NUMBER: US/9/594,119
; PRIOR FILING DATE: 1999-06-14
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver: 2.1
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; ORGANISM: Homo &
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                     CTGCAGCTGTGCCCCATCTGCAGAGCCCCCCCGTCCGCAGCCGCGTGCGCACCTTCCTGTCC
                                                                       AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGluCysAlaProGly
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GENERAL INFORMATION:
APPLICANT: Dranoff, Glenn
APPLICANT: Schmollinger, Jan
APPLICANT: Schmollinger, Jan
APPLICANT: Hodi, F. Stephen
APPLICANT: Hodi, F. Stephen
APPLICANT: Mollick, Joseph
TITLE OF INVENTION: TUWOR ANTIGENS AND USES THE
FILE REFERENCE: 50059/005W02
CURRENT APPLICATION NUMBER: PCT/US99/17738
CURRENT FILING DATE: 1999-06-06
EARLIER APPLICATION NUMBER: 60/095,766
EARLIER FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 11
LENGTH: 1246
TYPE: DNA
ORGANISM: Homo sapiens
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                      TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg
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Sequence 4, Application PC/TUS0320821
[GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
III'LE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXI-
FILE REFERENCE: ISISO37-500
[CURRENT APPLICATION NUMBER: PCT/US03/20821
[CURRENT FILING DATE: 2003-07-02
PRIOR APPLICATION NUMBER: US 10/188,646
[PRIOR PILING DATE: 2002-07-02
] PRIOR FILING DATE: 2002-07-02
[ NUMBER OF SEQ ID NOS: 153
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ORGANISM: H. sapiens
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(Sequence 27143, Application US/10170235
(SERERAL IMPORMATION:
(SENERAL IMPORMATION: VENTER, J. Craig
TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
(TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
(FILE REFERENCE: CLOROTISE)
(CURRENT APPLICATION NUMBER: US/10/170,235
(CURRENT FILING DATE: 2003-03-17
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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; GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXF
FILE REFERENCE: RTS-0373
; CURRENT APPLICATION NUMBER: US/10/188,646
; CURRENT EILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 4
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LOCATION: (174)...
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Matches:
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Sequence 11, Application US/10553355
GENERAL INFORMATION:
APPLICANT: Destsches Krebsforschungszentrum
TITLE OF INVENTION: Livin-specific siRNAs for the
FILE REFERENCE: DK62169PC
CURRENT APPLICATION NUMBER: US/10/553,355
CURRENT FILING DATE: 2005-10-14
PRIOR APPLICATION NUMBER: EP 0300 8081.6
PRIOR FILING DATE: 2003-04-15
NUMBER OF SEQ ID NOS: 11
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Homo :
US-10-553-355-11
                                                                                                                                                                                                                                                                             RESULT 7
US-10-553-355-11
                                                                     SEQ ID NO 11
                                                                                       SOFTWARE:
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RESULT 8
US-10-940-774-1949
; Sequence 1949, Application US/10940774
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
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CURRENT APPLICATION NUMBER: US/10/940,777,
CURRENT FILING DATE: 2004-09-15

PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/237, 768
PRIOR FILING DATE: 2000-09-08
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SEQUENCE 1949, Application US/10940774A

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF FILE REFERENCE: CL001307
CURRENT APPLICATION HUMBER: US/10/940,774A
CURRENT FILING DATE: 2004-09-15
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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APPLICANT: Mack, David H.
APPLICANT: Wilson, Keith E.
APPLICANT: Zlotnik, Albert
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-002710PC
CURRENT APPLICATION NUMBER: PCT/JS02/29560
CURRENT FILING DATE: 2025-11-01
PRIOR APPLICATION NUMBER: US 60/323,469
PRIOR FILING DATE: 2001-09-17
NUMBER OF SEQ ID NOS: 412
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 182
LENGTH: 1268
TYPE: DNA
ORGANISM: Homo Sapiens
PCT-US02-29560-182
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PCT-US02-29560-182
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APPLICANT: Aziz, Natash,
APPLICANT: Gish, Kurt C
APPLICANT: Hevezi, Pete:
APPLICANT: Mack, David I
APPLICANT: Wilson, Keitl
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GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
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SEQUENCE 182, Application PC/TUS0229560A

| SEQUENCE 182, Application PC/TUS0229560A
| GENERAL INFORMATION:
| APPLICANT: Afar, Daniel |
| APPLICANT: Afar, Daniel |
| APPLICANT: Herezi, Peter A. |
| APPLICANT: Wilson, Keith E. |
| APPLICANT: Zlotnik, Albert |
| APPLICANT: Eos Biotechnology, Inc. |
| TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and ITILE OF INVENTION: Methods of Screening for Modulators of CITLE REFERENCE: 018501-002710PC |
| CURRENT FILING DATE: 2001-09-17 |
| PRIOR APPLICATION NUMBER: PCT/US02/29560A |
| PRIOR FILING DATE: 2001-09-17 |
| SOFTWARE: FRESTEQ for Windows Version 3.0 |
| SEQ ID NO 182 |
| LEUGTH: 1268 |
| TYPE: DNA |
| ORGANISM: Homo sapiens |
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RESULT 12

PCT-US04-08932-28

; Sequence 28, Application F
; GENERAL INFORMATION:
; APPLICANT: Xiang, Rong
; APPLICANT: Zhou, He
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APPLICANT: The Scripps Research Institute
TITIZ OF INVENTION: DNA VACCINES AGAINST TUMOR GRC
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: TSR1-874.1PC
CURRENT APPLICATION NUMBER: PCT/US04/08932
CURRENT FILING DATE: 2004-03-29
FRIOR APPLICATION NUMBER: 60/457,009
PRIOR FILING DATE: 2003-03-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 1268
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                                                                                                                                                                                                        Score:
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                                                                                                                                                                                                                                                                  US-10-245-882-182
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US-10-245-882-182
                                                                                                                                                                                                                                                                          LENGTH: 1268
TYPE: DNA
ORGANISM: Homo:
                                                        174
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PRIOR APPLICATION NUMBER: US 60/372,246;
PRIOR FILING DATE: 2002-04-12;
NUMBER OF SEQ ID NOS: 412;
SOFTWARE: FastSEQ for Windows Version 3.0;
SEQ ID NO 182;
LENGTH: 1268;
Type- Fig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hevezi, Peter A.

APPLICANT: Mack, David H.

APPLICANT: Milson, Keith E.

APPLICANT: Zlotnik, Albert

APPLICANT: Zlotnik, Albert

ITILE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and

ITILE OF INVENTION: Methods of Diagnosis of Cancer

FILE REFERENCE: 018501-002710US

CURRENT APPLICATION NUMBER: US/10/245,882

CURRENT FILING DATE: 2002-12-13

PRIOR APPLICATION NUMBER: US 60/323,469

PRIOR FILLING DATE: 2001-09-20

PRIOR APPLICATION NUMBER: US 60/323,887

PRIOR APPLICATION NUMBER: US 60/323,887

PRIOR APPLICATION NUMBER: US 60/325,114

PRIOR FILLING DATE: 2001-09-20

PRIOR APPLICATION NUMBER: US 60/325,114

PRIOR FILLING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: US 60/340,944

PRIOR FILLING DATE: 2001-10-29

PRIOR APPLICATION NUMBER: US 60/350,666

PRIOR APPLICATION NUMBER: US 60/350,666

PRIOR APPLICATION NUMBER: US 60/355,145

PRIOR APPLICATION NUMBER: US 60/355,145

PRIOR APPLICATION NUMBER: US 60/355,145

PRIOR FILLING DATE: 2002-02-08

PRIOR FILLING DATE: 2002-02-08

PRIOR APPLICATION NUMBER: US 60/359,899

PRIOR APPLICATION NUMBER: US 60/369,899

PRIOR APPLICATION NUMBER: US 60/369,899

PRIOR APPLICATION NUMBER: US 60/369,899
                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                        US-09-762-577B-12 (1-309) x US-10-245-882-182 (1-1268)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natash
APPLICANT: Gish, Kurt C
APPLICANT: Hevezi, Pete
APPLICANT: Mack, David I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 182, Application GENERAL INFORMATION:
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AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu
                                                                                    MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla
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                                                                ATGGGACCTAAAGACAGTGCCAAGTGCCTGCACCGTGGACCACAGCCGAGCCACTGGGCA
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Gish, Kurt C.
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Matches:
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Sequence 28, Application US/10807897

Sequence 28, Application US/10807897

APPLICANT: Xiang, Rong

APPLICANT: Xiang, Rong

APPLICANT: Reisfeld, Ralph A.

APPLICANT: The Scripps Research Institute

TITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GROWTH AND

TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: TSR1-874, 1

CURRENT APPLICATION NUMBER: US/10/807,897

CURRENT FILING DATE: 2004-03-24

PRIOR APPLICATION NUMBER: 60/457,009

PRIOR FILING DATE: 2003-03-24

INUMBER OF SEQ ID MOS: 29

SEQ ID NO 28

LENGTH: 1268

TYPE: DNA

ORGANURS:

NAME/KEY: CDS

LOCATION: (174)...(1016)
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RESULT 15
US-60-685-372-1181
; Sequence 1181, Application
; GENERAL INFORMATION:
; APPLICANT: Belouchi, Abdel
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; ORGANISM: Homo
US-60-685-372-1181
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APPLICANT: Cousineau, Johanne
APPLICANT: Berdewegh, Paul V
APPLICANT: Segal, Jonathan
TITLE OF INVENTION: Genemap of the Human Genes Associated with Psoriasis
FILE REFERENCE: 059908-5005-PR
CURRENT APPLICATION NUMBER: US/60/685,372
CURRENT FILING DATE: 2005-05-31
NUMBER OF SEQ ID NOS: 2738
SOFTWARE: Patentin version 3.3
SEQ ID NO 1181
LENGTH: 1268
TYPDE. TNN
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Nguyen-Huu, Quynh
Croteau, Pascal
Allard, Rene
                                          GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu
                                                                             AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
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LeuProThrProArgArgGluValGlnSerGluSerAlaGlnGluProGlyAlaArgAsp
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Bradley, Walter E
Paquin, Bruno
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Search completed: April 24, 2006, 11:51:02 Job time : 6656 secs

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Result
No.
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-Q=/abss/ABSSWEB_spool/US09762577/runat_24042006_105934_1148/app_query.fasta_1
-Da-bending_Patents_NA_New -QFMT=fastap_-SUFFIX=p2noli.rnpn -MINWATCH=0.1
-DOPCL=0 - LOOPEXT=0 - UNITS-bits -START=1 - END=-1 -MATRIX=01igo
-TRANS=human40.cdi - LIST=45 - DOCALIGN=200 - THR SCORE=quality - THR MIN=1
-ALIGN=15 - MODE=LOCAL - OUTFMT=pco -NORM=ext - HEARSIZE=500 -MINLEN=0
-MAXLEN=200000000 - HOST=abss03p
-USER-US09762577 @CGN 1_1 803 @runat 24042006_105934_1148 -NCPU=6 -ICPU=3
-NO MMAP - NCE_SCORES=0 - WAIT - TOSPBLOCK=100 - LONGLOG -DEV_TIMEOUT=120
-NARN_TIMEOUT=30 - THREADS=1 - XGAPOP=60 - XGAPEXT=60 - FGAPOP=60 - FGAPEXT=7
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                                                                                                          Score
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1: /SIDS5/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /SIDS5/ptodata/2/pna/US06_NEW_COMB.seq:*

3: /SIDS5/ptodata/2/pna/US07_NEW_COMB.seq:*

4: /SIDS5/ptodata/2/pna/US09_NEW_COMB.seq:*

4: /SIDS5/ptodata/2/pna/US10_NEW_COMB.seq:*

6: /SIDS5/ptodata/2/pna/US10_NEW_COMB.seq:*

7: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq:*

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Ygapop 60.0,
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Match Length DB
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US-11-266-748A-290500
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Sequence 11, Appl
Sequence 23550, A
Sequence 290500,
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ALIGNMENTS

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RESULT 1

US-09-762-577B-11

US-09-762-577B-11

J Sequence 11, Application US/09762577B

GENERAL INFORMATION:

APPLICANT: Dranoff, Glenn

APPLICANT: Hodi, F. Stephen

CURRENT APPLICATION ITHMOR ANTIGENS AND USES THEREOF

FILE REFERENCE: 2486/109

CURRENT FILING DATE: 2002-08-29

FRIOR APPLICATION NUMBER: 60/095,766

PRIOR APPLICATION NUMBER: 60/095,766

PRIOR APPLICATION NUMBER: 60/095,766

PRIOR APPLICATION NUMBER: 60/095,766

PRIOR FILING DATE: 1998-08-07

J NUMBER OF SEQ ID NOS: 68

SOFTWARE: FASTSEQ for Windows Version 4.0

J SEQ ID NO 11

LENGTH: 1246

TYPE: DNA

ORGANISM: homo sapiens

US-09-762-577B-11

Alignment Scores:

Pred. No.:

280.00

Percent Similarity: 100.0%

Best Local Similarity: 100.0%

Matches: 0
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RESULT 2
US-11-266-748A-23550
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  Sequence 2350, Application US/11266748A
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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Best Local Similarity:
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PRIOR FILING DATE: 2004-11-03
PRIOR PPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PRIOR DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
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SOFTWARE: PatentIn version 3.
SEQ ID NO 23550
LENGTH: 1260
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILLNG DATE: 2005-11-03
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PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
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PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105486.9
PRIOR APPLICATION NUMBER: EP 04105484.2
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US-11-266-748A-290500
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US-11-266-748A-290500
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SEQ ID NO 290500
LENGTH: 1000
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GENERAL INFORMATION:
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PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
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                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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US-11-266-748A-341929/c
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NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3
SEQ ID NO 341929
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APPLICANT: Johnston, F
APPLICANT: Mulligan, K
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TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: ED 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR PELICATION NUMBER: ED 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: ED 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: ED 04105485.9
PRIOR APPLICATION NUMBER: ED 04105484.2
PRIOR APPLICATION NUMBER: ED 04105484.2
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: ED 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: ED 04105484.2
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: ED 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
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Mulligan, Karl
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RESULT 5
US-11-266-748A-211754/c
// Sequence 211754, Application U
// GENERAL INFORMATION:
// APPLICANT: Harkin, Paul
// APPLICANT: Johnston, Patrick
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; TYPE: DNA
; ORGANISM: Homo Sapiens
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Mismatches:
Indels:
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RESULT 6
US-11-266-748A-235360
US-11-266-748A-235360, Application US/11266748A
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray
TITLE OF INVENTION: Methods of Using the Sar
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ITILE OF INVENTION: Transcriptome Microarray Technology and
ITILE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: US 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PILING DATE: 2005-07-18
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DB:
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Best Local Similarity:
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Microarray Technology

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-235360
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PPLICATION NUMBER: EP 04105483.4
PRIOR PPLICATION NUMBER: EP 04105507.0
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PATENTIN VETSION 3.3
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Sequence 49, Application US/09762577B
GENERAL INFORMATION:
APPLICANT: Dranoff, Glenn
APPLICANT: Schmollinger, Jan
APPLICANT: Hodi, F. Stephen
APPLICANT: Mollick, Joseph
TITLE OF INVENTION: TUMOR ANTIGENS AND USES THEREOF
FILE REFERENCE: 2486/109
CURRENT APPLICATION NUMBER: US/09/762,577B
CURRENT FILING DATE: 2002-08-29
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LENGTH: 633
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
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; NAME/KBY: misc feature
; LOCATION: 163, 168
; OTHER INFORMATION: n = A
US-09-762-577B-49
                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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US-11-266-748A-41998
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Best Local Similarity:
Query Match:
DB:
   US-09-762-577B-12 (1-309) x US-11-266-748A-41998 (1-634)
                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo S
US-11-266-748A-41998
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PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 49
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                                                                                                                                                                                                                                                                                                                                              LENGTH: 63
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TYPE: DNA
ORGANISM: homo sapiens
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Alignment Scores:

RESULT 7 US-09-762-577B-49

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Percent Similarity:
Best Local Similarity:
Query Match:
                                                     US-09-762-577B-12 (1-309) x US-11-266-748A-15520 (1-927)
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US-11-266-748A-15520
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PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR PILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PILING DATE: 2005-07-18
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SEQ ID NO 15520
LENGTH: 927
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILLING DATE: 2005-11-03
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APPLICANT: Johnst
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OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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LOCATION: (712)..(712)
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224 GlnLeuArgArgLeuGlnGluGluArgThrCysLysValCys
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PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 0405484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR PILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PILING DATE: 2005-07-18
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Best Local Similarity:
Query Match:
RESULT 11
                                                                                                            US-09-762-577B-12 (1-309) x US-11-266-748A-21170 (1-927)
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US-11-266-748A-21170
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GENERAL INFORMATION:
APPLICANT: Harkin, Paul
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NAME/KEY: misc_feature

TOCATION: (887)...(887)
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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NAME/KEY: misc feature
LOCATION: (641)..(696)
OTHER INFORMATION: n is
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ORGANISM: Homo Sapiens
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APPLICANT: JOHNSTON, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.7
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US-11-266-748A-115538
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Best Local Similarity:
Query Match:
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US-11-266-748A-13769
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PRIOR FILING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 055-07-18
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Wethods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.3
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9 PRIOR FILING DATE: 2004-11-03 PRIOR APPLICATION NUMBER: EP 04105484.2 PRIOR FILING DATE: 2004-11-03
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/866,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
                                                                                                                                                                                                        ; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-157702
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US-09-762-577B-12 (1-309) x US-11-266-748A-157702 (1-1000)
                                                                                 Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
Query Match:
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; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-115538
                                                                                                                                                                     Alignment Scores:
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                                                                                                                                                                                                                                                                                          SOFTWARE: Patent
SEQ ID NO 157702
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 115538
LENGTH: 1000
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APPLICANT: Johnston, P
APPLICANT: Mulligan, K
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PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 483996
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                                                                                                                                                 No.:
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FILING DATE: 2004-11-03
APPLICATION NUMBER: EP 04105484.2
FILING DATE: 2004-11-03
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Matches:
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224 GlnLeuArgArgLeuGlnGluGluArgThrCysLysValCys 237

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US-11-266-748A-220957

Sequence 220957, Application US/11266748A

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Johnston, Patrick

APPLICANT: MU11igan, Karl

TITLE OF INVENTION: Transcriptome Microarray Technology and

TITLE OF INVENTION: Methods of Using the Same

FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.9

PRIOR APPLICATION NUMBER: EP 04105484.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: US 60/662,276

PRIOR FILING DATE: 2005-03-14

PRIOR APPLICATION NUMBER: US 60/700,293

PRIOR FILING DATE: 2005-07-18

NUMBER OF SEO ID NOS: 483996
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
ITILE OF INVENTION: Transcriptome Microarray Technology and
ITILE OF INVENTION: Methods of Using the Same
FILE REFERENCE: $5815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105403.4
PRIOR APPLICATION NUMBER: EP 04105507.0
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Query Match:
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; ORGANISM: Homo Sapiens
US-11-266-748A-220957
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GENERAL INFORMATION:
APPLICANT: Harkin, Paul
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Search completed: April 24, Job time: 2339 secs
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Query Match:
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US-11-266-748A-224572
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PRIOR FILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILLING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILLING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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SEQ ID NO 224572
LENGTH: 1000
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                           178 CAATTGCGGAGACTACAAGAAGAAGAACATGTAAAGTGTGT 219
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